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(54) **DIFFERENTIALLY-EXPRESSED CONIFER CDNAS, AND THEIR USE IN IMPROVING SOMATIC EMBRYOGENESIS**

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(51) **Int. Cl.**
G06F 19/00 (2006.01)
C12Q 1/68 (2006.01)
C12N 15/29 (2006.01)

(52) **U.S. Cl.** **702/19**; 435/6; 536/24.3

(58) **Field of Classification Search** 536/23.1; 435/6

See application file for complete search history.

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(57) **ABSTRACT**

The invention relates to a method for staging embryos of plants. In particular, this invention relates to a method for creating a relational database by determining transcript levels of sets of genes expressed at predetermined stages in embryo development. This approach creates a method by which embryos of unknown stage development can be determined by comparisons between expression levels of those embryos to the expression levels found in the database. This approach further allows rapid identification of transcripts in an embryo to be staged by the utilization of probes corresponding to cDNAs comprising the database. Additionally, this invention relates to a method for selecting advantageous plant clones for future propagation. Specifically, this method relates to an approach to link the biochemical condition of an embryo to current culture conditions and thus provides a method for enhancing conditions to produce embryos with a desired biochemical state.

7 Claims, 14 Drawing Sheets

FiGURE 1

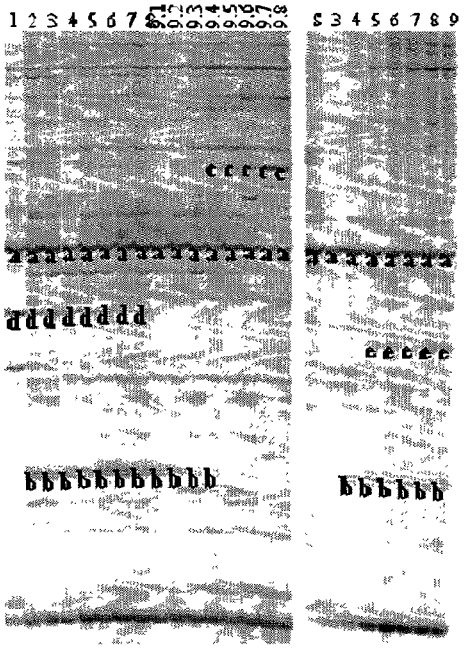


Figure 1. Differential display of loblolly pine zygotic and somatic embryos at different stages of development. The zygotic embryos (left panel) used were from tree BC-1 and the somatic embryos (right panel) are of genotype 260. Primer pair T12VC-AP3 (GenHunter, Nashville, TN) were used in the PCR reactions. The numbers on the top of the lanes indicate the stages of the embryos used. The letters superimposed on the images mark different types of banding patterns: (a), the band appeared in both embryos at all the stages; (b), early to middle stages in ZE and middle to late stages in SE; (c), late stages in ZE and absent in SE; (d), early stages in ZE and absent in SE; (e), present in SE but not in ZE.

FIGURE 2

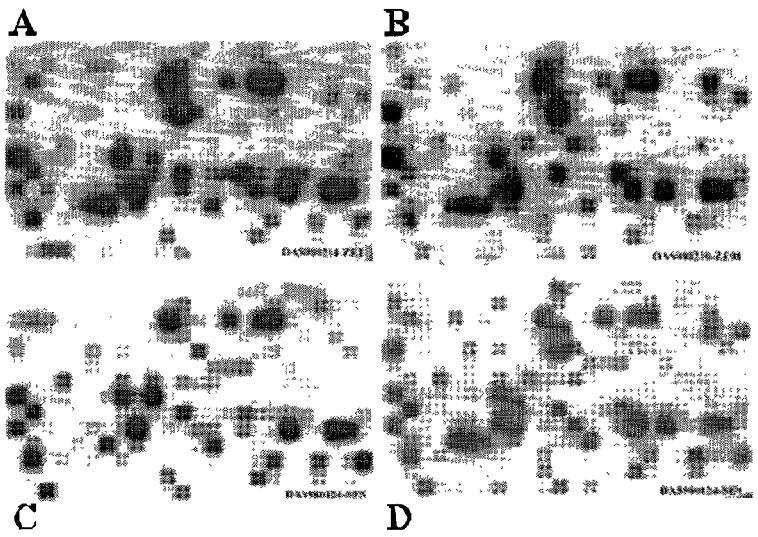


Figure 2. Detection of gene expression by high-density array Southern hybridization. Cloned cDNAs (327) were blotted on a membrane as high-density arrays. Each cDNA was blotted four times as a quadrate. The membranes were hybridized to the total cDNAs derived from total mRNA isolated from zygotic embryos at stage 1 (A), stage 9.8 (B), somatic embryos at suspension stage (C), and stage 9 (D). Dark spots indicate high level of gene expression and light spots indicate low level of gene expression.

FIGURE 3

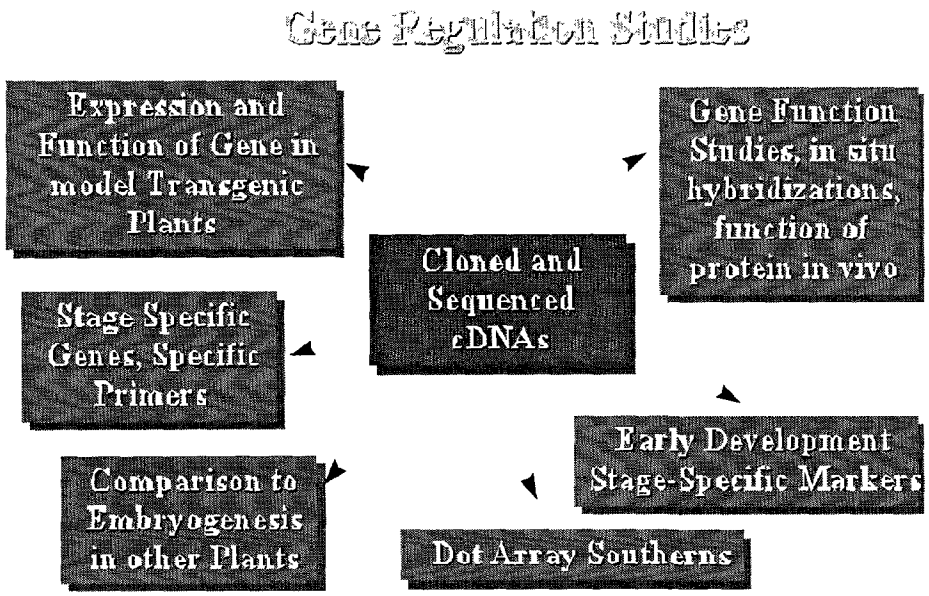


Figure 3. Gene regulation studies arising from the cDNA cloning of genes expressed in embryos. See text for their applicability to process improvement.

FIGURE 4

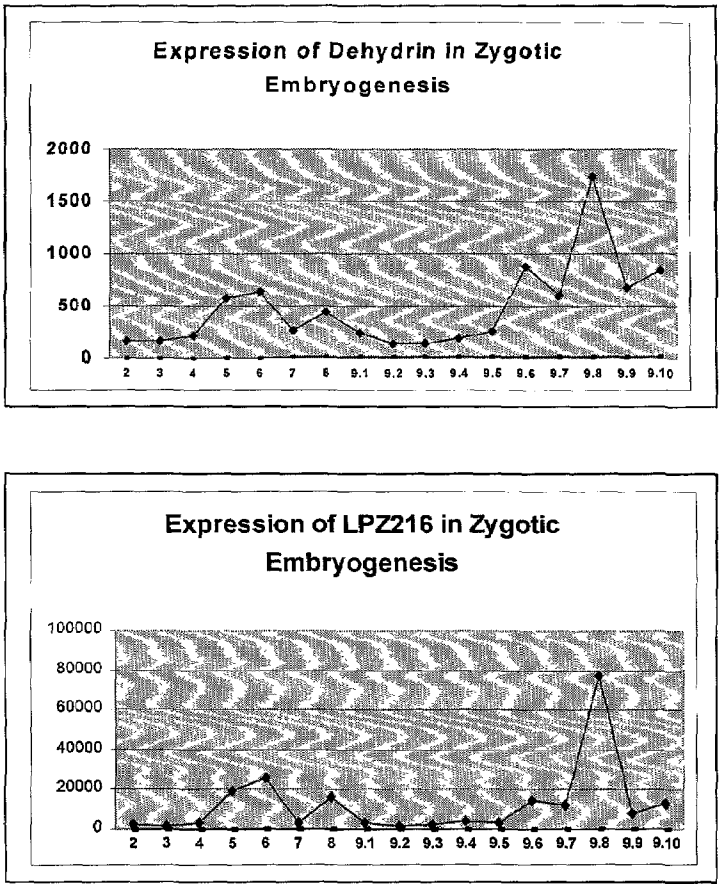


Figure 4. Graphical representation of hybridization of 'dehydrin' and LPZ-216 cDNA probes to total RNA isolated from zygotic embryos of loblolly pine. Five micrograms of RNA was loaded on a slot blot and hybridized with one of the cDNA probes. The hybridization signals were measured by a Fuji BAS-1000 Imaging system and signals were quantified using the associated software. The membrane was then stripped of probe and re-probed with labeled 26S rDNA to determine the equivalence of loading. These signals from this hybridization were captured and used to normalize the signals from dehydrin and LPZ-216.

FIGURE 5

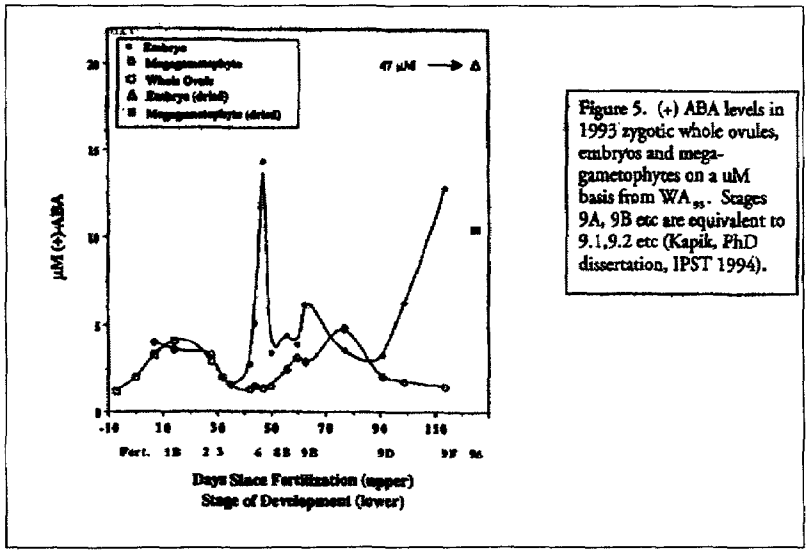


Figure 5. Determination of ABA concentration of loblolly pine embryos as described more fully by Kapik et al., *Tree Physiology* 15:485-490 (1995)

FIGURE 6

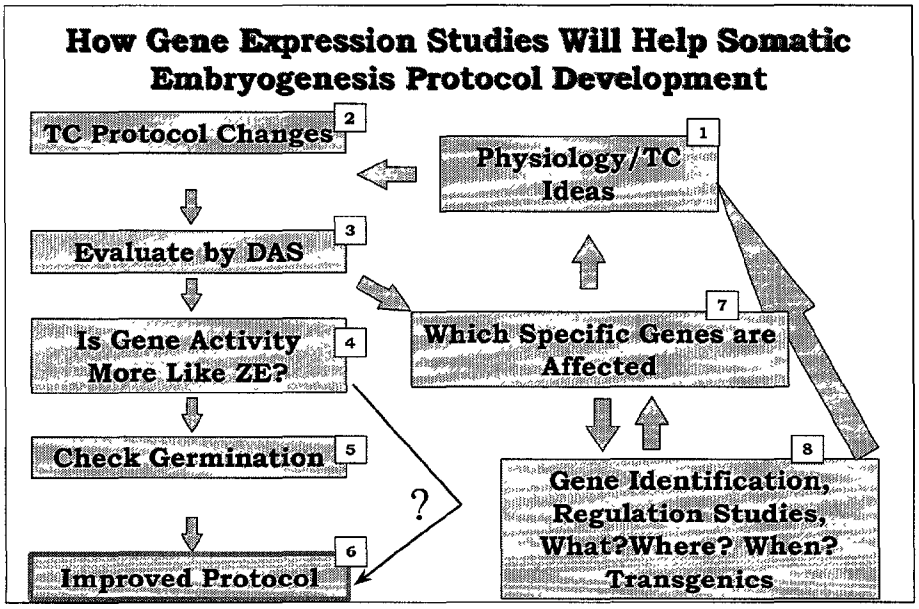


Figure 6. Scheme showing use of gene studies to improve somatic embryogenesis. **TC = Tissue Culture, DAS = DNA Array Southern (an expression monitoring technique), ZE = Zygotic (Natural) Embryo**

FIGURE 7

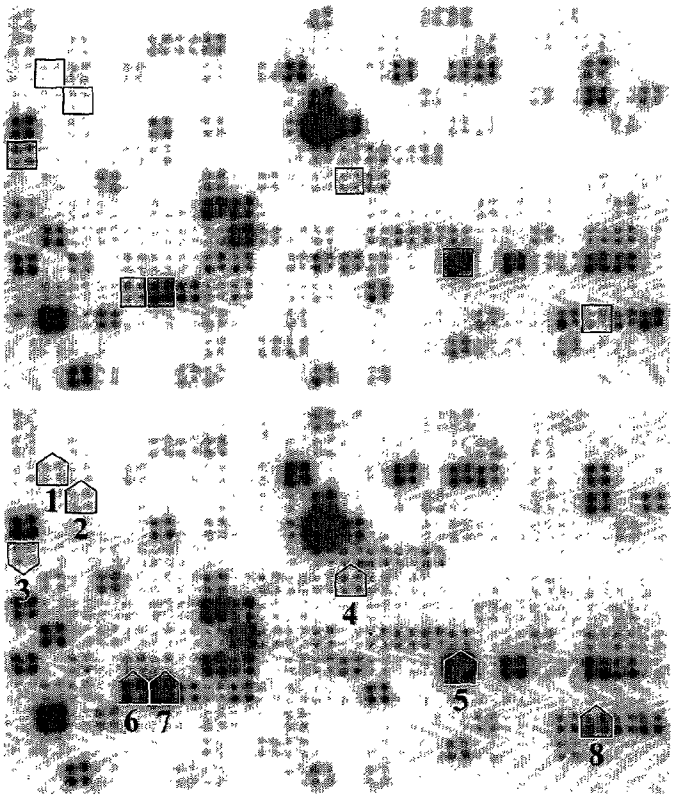


Figure 7. Detection of gene expression by high density array Southern hybridization for loblolly pine genotype 333 after 12 weeks on two maturation media. Top, 5.2 mg/L ABA; bottom 10 mg/L ABA. Arrows up indicate increased gene expression in the 10 mg ABA treatment; arrow down, expression lower in 10 mg ABA treatment. Squares in top panel mark the corresponding spots marked in the bottom panel. Gene 1 (LPS-064), expression is usually higher in ZE than in SE; 2 (LPS-092) expressed in late ZE; 3 (LPZ-049) is starch synthase, higher level in ZE; 4 (LPZ-091) LMW heat shock protein, found in late stage ZE; 5 (LPZ-202) lea gene (late embryo abundant); 6 (LPZ-215) higher level in late ZE; 7 (LPZ-216) lea gene; 8 (LPZ-270) 70S heat shock protein, found in late ZE. A lower level of #3 means a decreased synthesis of starch in 10 mg ABA treatment. All the others bring the expression closer to ZE.

FIGURE 8

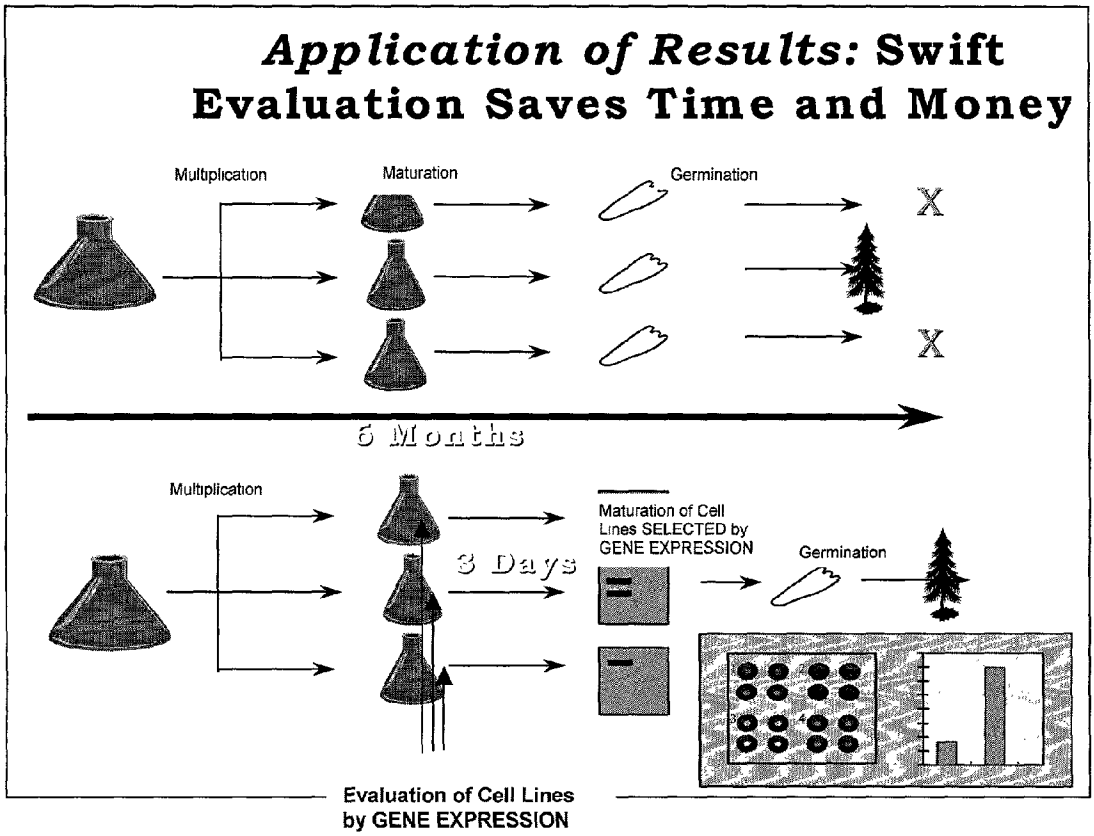
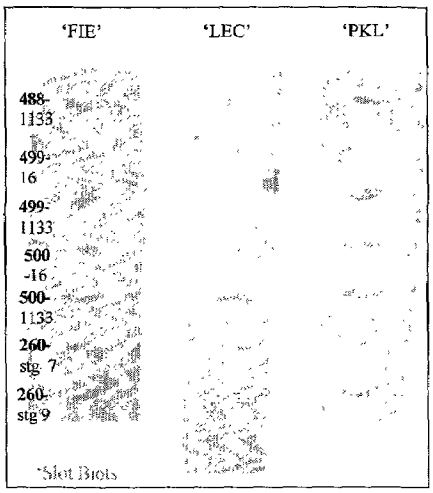


Figure 8. Application of results.

FIGURE 9

A.



B.

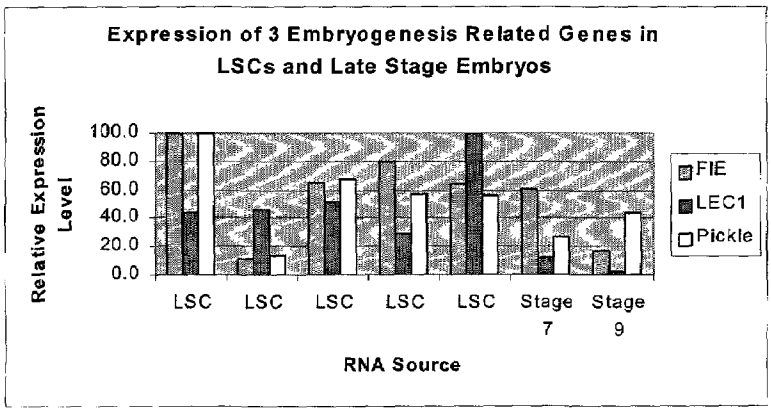


Figure 9. a. Image of RNA slot blot probed with pine cDNA clones bearing similarity to the 'fie' 'lec' or 'pkl' genes from Arabidopsis thaliana. Two micrograms of Loblolly Pine RNA, extracted from either liquid suspension culture (somatic embryos, stage1 &2) or from somatic embryos stage 7 or stage 9, were blotted using a slot blot manifold (Hoeffer ScientificInsturments, San Francisco) according to manufacturers instructions onto Hybond™ N+ (Amersham Pharmacia Biotech, Piscataway, NJ, USA) and UV crosslinked. Each of the three membranes contains identical amounts of the same RNA. The numbers in bold on the left hand side of the images refer to the genotype of the cell line, the numbers below the genotype refer to the media in which embryos were cultured. B. Quantification of the signals shown in panel 9a. Blots were exposed to a phosphorimaging plate for 10 minutes. Screens were read with a BAS1800 (software v1.0) and images were manipulated with ImageGauge (v2.54) (Fuji Photo Film Co., Ltd., Kanagawa, Japan).

FIGURE 10

GGGCACAAAGCTCCGCAGCCTGAGCGAGCGTCATTAGCTTGTCAGTCGGAACCAT

TACCCCTTTCCTCTTCGCTGGCTAGCGAATGATAGGGAATGCTAGCCAGCGAACAA

GATTAGAGCACAGAAAGTATAGCCAGCGAATCAACAGCATAACAACTTAGAGATTTCTTGCAT

TCCCCAGACGGTATCAAGTCATAGTGGAGAATAATCATAATAAGATTTGTGAAAATG

TTTGTGTAGATTAATGTGTAAAATTCAATCCATCAACCATGAAGTGAAGTGCATTCCGTTTTTAA

ATGTTTATTGTATTTGAATGAATAAACAGTTTACACGCGAAAATCCCTACTTTATGTG

CGTACAAACTATGATTTTTTTTGCAGTATATAAAAGTTTCCACTATCGTAATTATTTTC

CAGATCCGTCTTCTTAACAACCCGATTTCCTAGCATCCATCTGCGTGGAATAAATCT

ATTGAATTATTAACCCTTGTGATTGGCTAAAAAAAAAA

Figure 10. Sequence of LP2-3 differential display fragment, 507 nucleotides, clone LPS-097.

FIGURE 11

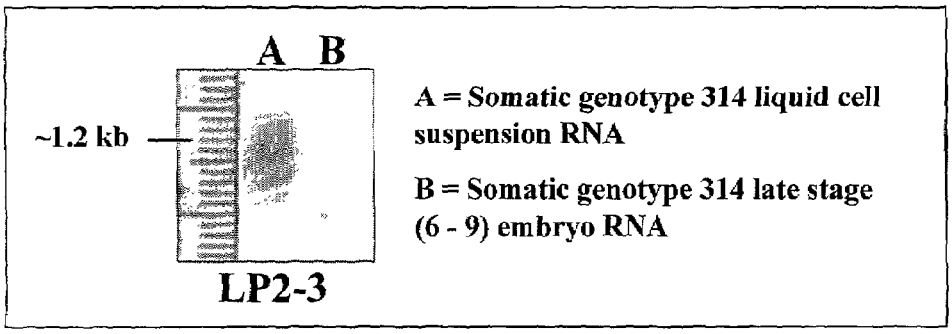
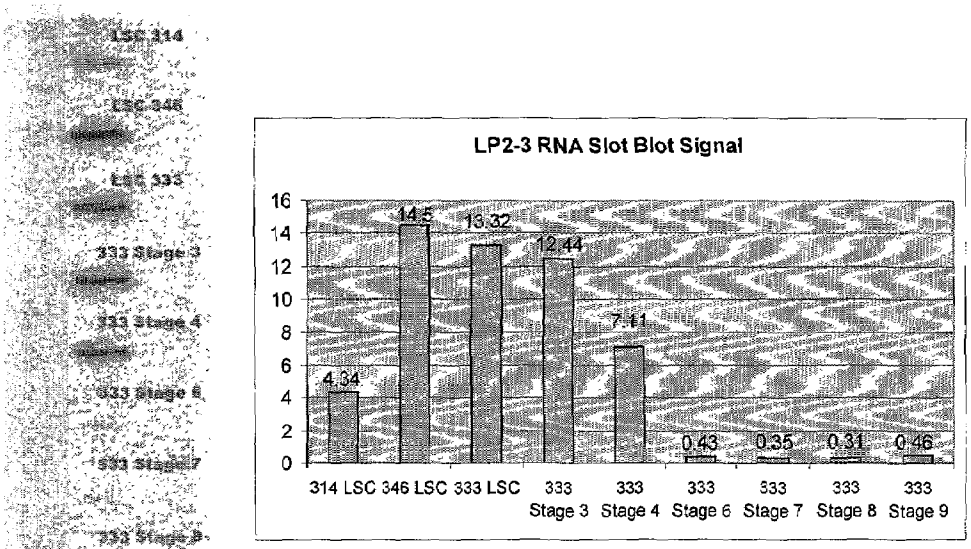


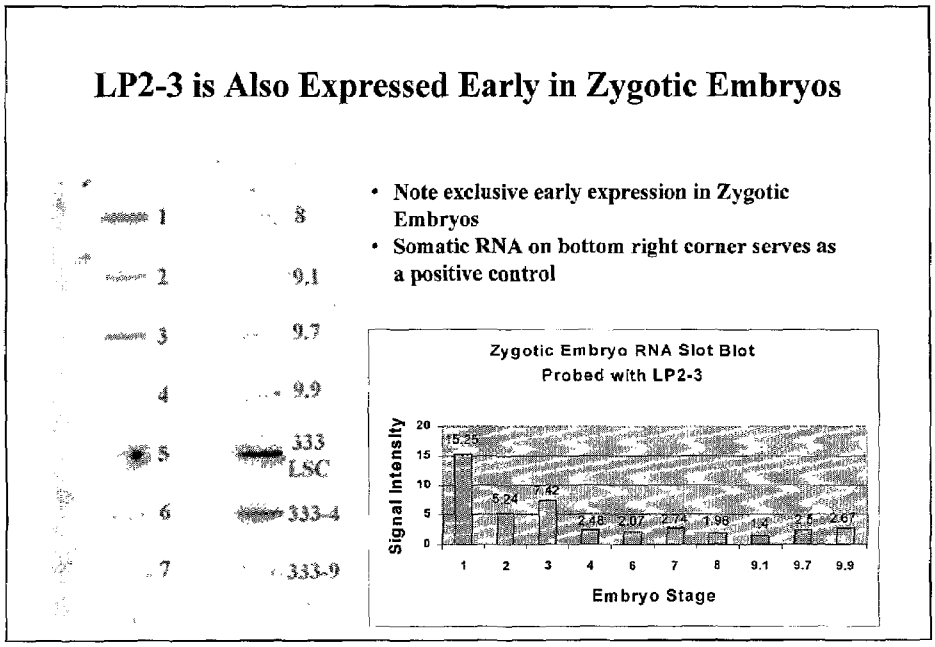
Figure 11. Expression of LP2-3 Gene: Northern Blot of total RNA isolated from Liquid Suspension Culture (Stages 1-3) and Late Stage (Stage 9) Loblolly Pine Somatic Embryos (Pullman & Webb 1994).

FIGURE 12



Figures 12A & 12B. Image (1A) and quantification (1B) of a total RNA slot blot probed with an LP2-3-specific probe. For each somatic embryo tissue (liquid suspension culture (LSC) genotypes 314, 346, and 333, and genotype 333 stages 3, 4, 6, 7, 8, and 9) two micrograms of total RNA was attached at each position on the membrane. This blot shows that LP2-3 mRNA is most abundant in early stage somatic embryos, especially when they are in the liquid multiplication medium, and decreases rapidly as embryos begin to mature on maturation medium. It is also apparent that when comparing genotypes, there is variability in LP2-3 abundance in LSC.

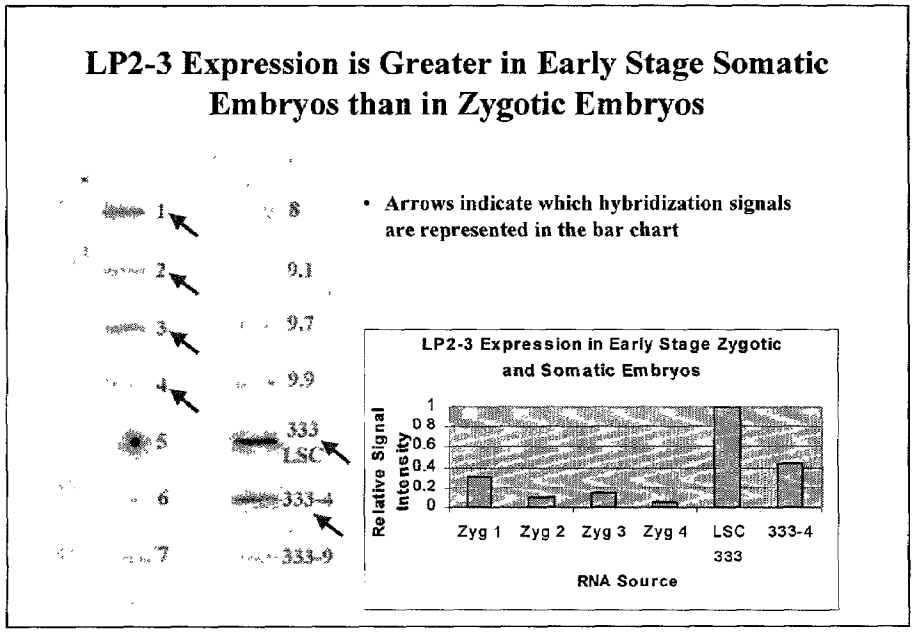
FIGURE 13



A B

Figures 13A & 13B. Image (A) and quantification (B) of a total RNA slot blot probed with an LP2-3-specific probe. Isolation of zygotic embryos used in this experiment. From June to September 1996, open-pollinated cones were collected from Union Camp mother tree UC5-1036 were packed on ice and shipped overnight to IPST. Seeds were removed from cones, cracked with a hemostat, and dissected with scalpel and forceps. From each seed the intact ovule was extracted and the megametophyte was sliced open. Embryos were removed, visually judged for stage of development (Pullman & Webb 1994), plunged into liquid nitrogen and stored (20 embryos per 2 mL cryogenic vial (Nalgene Cat. No. 5000)) at -70°C. For somatic embryos, liquid suspension tissue (LSC) was collected, dried by squeezing gently in miracloth (Behring Diagnostics), plunged into liquid nitrogen, and stored at -70°C. Similarly, later stage somatic embryos were plucked from culture, assessed for stage of development, plunged into liquid nitrogen, and stored in vials of 20 to 25 embryos at -70°C.

FIGURE 14



A B

Figures 14A & 14B. Image (A) is as shown in Fig. 13A. The quantified expression of early stage zygotic embryos compared to early stage somatic embryos shown in Fig. B

DIFFERENTIALLY-EXPRESSED CONIFER CDNAS, AND THEIR USE IN IMPROVING SOMATIC EMBRYOGENESIS

CROSS-REFERENCE TO RELATED APPLICATIONS

This patent application claims benefit of priority of provisional application U.S. Ser. No. 60/239,250, filed Oct. 11, 2000, and claims benefit of priority of provisional application U.S. Ser. No. 60/260,882, filed Jan. 12, 2001.

FIELD OF THE INVENTION

The present invention relates to a relational database of cDNA molecules, including those corresponding to Loblolly Pine Major Intrinsic Protein (MIP), which are differentially expressed during plant embryogenesis. The present invention further relates to the use of DNA arrays for evaluating gene expression in somatic and zygotic embryos. The invention encompasses related nucleic acids, proteins, antigens, and antibodies derived from these cDNAs as well as the use of such molecules for the staging, characterization, and manipulation of plant embryogenesis, in particular conifer embryogenesis. The cDNAs and related nucleic acids, proteins, antigens, and antibodies derived from these cDNAs are useful in the design, selection, and cultivation of improved crops, specifically including coniferous trees, which provide raw materials for paper and wood products.

BACKGROUND OF THE INVENTION

The world demand for paper is expected to increase nearly 50% by the year 2010 (McNutt and Rennel, *Pulp Paper Intern* 39: 48 (1997)). The United States' forest products industry faces a great challenge in order to keep pace with the growing demand for paper. This challenge is made greater by the decreasing availability of a forest land-base, resulting from environmental restrictions and urban growth, from which to harvest timber resources. Additionally, valuable wood resources are lost to the environmental stresses and biotic diseases. Consequently, the push to secure a renewable and sustainable source of raw material for paper and other wood related products has become an important priority for the forest products industry.

Current forestry related research and development is focused on creating sustainable fiber farms or tree plantations. Farming trees with elite germplasms will increase growth rates and yields of wood per acre. However, creating improved tree stock requires the ability to identify and generate genetically superior trees and a way to propagate such superior trees without diluting their genetic quotient.

A. Breeding and Selection

Addressing the need to propagate genetically superior trees without genetic diminution demands full research attention. Traditional methods of tree propagation relied on selected breeding programs to achieve genetic gain, i.e., the development of a strain, sub-strain, or line having any heritable and economically valuable characteristic or combination of characteristics not found in the parents. Based on the results of progeny tests, superior maternal trees are selected and used in "seed orchards" for mass production of genetically improved seed. The genetic gain in such an open-pollinated sexual propagation strategy is, however, limited by the breeder's inability to control the paternal

parent. Additional gains can also be achieved by control-pollination of the maternal tree with pollen from individual trees whose progeny have demonstrated superior growth characteristics. Nevertheless, even under controlled conditions where both parents of each seed are the same, sexual propagation results in a "family" of seeds, i.e., siblings, comprised of many different genetic combinations. As not all genotype combinations are favorable, the genetic gain in any particular progeny is frequently offset and obscured by the genetic variation among sibling seeds and those seedlings retaining undesirable or previously masked pre-cross traits.

In addition to inherent genetic limitations of a traditional breeding programs, large-scale production of control pollinated seeds is also expensive. Consequently, economic and biological limitations of large-scale seed production has lead the industry to turn towards methods of asexual reproduction, such as grafting, vegetative propagation and micropropagation, as more viable alternatives.

B. Asexual (Clonal) Propagation

Asexual propagation permits the application of very high selection intensity, resulting in the propagation of only those progeny showing a high genetic gain potential. These highly desirable progeny can have unique genetic combinations that result in superior growth and performance characteristics. Thus, with asexual propagation it is possible to genetically select individuals while avoiding a concomitant reduction of genetic gain due to intra-familial variation.

Asexual propagation of trees can be accomplished currently by grafting, vegetative propagation, and micropropagation. Grafting, widely used to propagate select individuals in limited quantities for seed orchard establishment, is not applicable to large-scale production for reforestation. Vegetative propagation, achieved by the rooting of cuttings, and micropropagation by somatic embryogenesis, currently hold the most potential for reforestation of conifers. Although vegetative propagation by rooted cuttings can be achieved in many coniferous species, large-scale production via this method is extremely costly due to difficulties in automating and mechanizing the process, not to mention the need for tremendous quantities of stock tissue. This propagation method is still further limited by the fact that the rooting potential of stock plants decrease with time, making it difficult to serially propagate from select genotypes over extended periods of time.

Micropropagation is the most promising method of asexual propagation for mass plantings. This process involves the production of somatic embryos in vitro from minute pieces of plant tissue or individual cells. The embryos are referred to as somatic because they are derived from the somatic (vegetative) tissue, rather than from the sexual process. Both vegetative propagation and micropropagation have the potential to capture all genetic gain of highly desirable genotypes. However, unlike conventional vegetative propagation methods, somatic embryogenesis is amenable to automation and mechanization, making it highly desirable for large-scale production of planting stock for reforestation. Moreover, somatic embryogenesis is particularly amenable to high intensity selection of a large number of clones. These advantages are compounded by the ability to safely preserve somatic embryogenic cultures in liquid nitrogen for long-term storage. Consequently, long-term cryogenic preservation offers immense advantages over other vegetative propagation systems that attempt to maintain the juvenility of stock plants. Techniques for somatic embryogenesis in a wide variety of plant species are

well known in the art; exemplary methods for performing somatic embryogenesis in conifers are taught in U.S. Pat. Nos. 5,036,007; 5,236,841; 5,294,549; 5,413,930; 5,491,090; 5,506,136; 5,563,061; 5,677,185; 5,731,203; 5,731,204; and 5,856,191, herein incorporated by reference in their entirety.

Thus, somatic embryogenesis has great potential for clonal production of conifer embryos to meet the increased demands of the pulp and paper industry. Assessment of embryo quality, however, needs improvement. The process of creating better tree stock begins with understanding the process of tree development from embryogenesis through full maturation.

In general, plant tissue culture is the broad science of growing plant tissues on or in a nutrient medium containing minerals, sugars, vitamins and plant hormones. By adjusting the composition of the media, cultured tissues can be induced to grow or differentiate into specific cell types or organs. "Somatic embryogenesis" is a type of plant tissue culture where a piece of a donor plant is excised, cultured and induced to form multiple embryos. An embryo is a discrete mass of cells with a well-defined structure that is capable of growing into a whole plant.

The methods generally in use for somatic embryogenesis today involve several steps. Prior to the tissue culture process, a suitable "explant" is harvested. A typical explant in conifer somatic embryogenesis is the "megagametophyte", a haploid nutritive tissue of the conifer seed, which is extracted from the ovule of a pollinated female cone. This ovule contains single or multiple zygotic seed embryos. In the seeds of many coniferous species, one or more genetically unique embryos naturally undergo a process called cleavage polyembryony, where a zygotic embryo grows and divides to form a small clones of embryos.

The first step in somatic embryogenesis is the initiation step. The explant is placed on a suitable media. When the explant is an ovule, a process called extrusion occurs. Extrusion involves the emergence or expulsion of a zygotic embryo or multiple embryos and embryogenic tissue out of the megagametophyte. If culture conditions are suitable, initiation proceeds and the extruded embryo or embryos undergo the process of cleavage polyembryony. This results in the formation of early stage somatic embryos in a glossy, mucilaginous mass.

After embryogenic cultures are initiated, the somatic embryos are transferred to a second medium with an appropriate composition of plant hormones and other factors to induce the somatic embryos to multiply. In the multiplication stage, cultures can double up to 2–6 times in one week. Once large numbers of embryos are obtained in the multiplication stage, the embryos are moved to a development and maturation medium. Here, the correct balance of plant hormones and other factors will induce the early-stage embryos to mature into late stage embryos. Following the maturation and development stage, embryos are germinated to form small seedlings. These seedlings are then acclimated for survival outside of the culture vessel. After acclimation, the seedlings are ready for planting.

The relative ability to propagate plants by somatic embryogenesis can vary greatly between species. Among conifers, for example, spruce (*Picea*) species and Douglas fir are easily propagated, while *Pinus* species are much more difficult. Many *Pinus* species, including Loblolly pine (*Pinus taeda*), do not readily initiate embryonic cultures. Typical initiation frequencies between 1% and 12% are reported for various *Pinus* species (Becwar et al., *For. Sci.* p1–18 (1988), Jain et al., *Plant Sci.* 65:233–241 (1989), Becwar et al., *Can. J. For. Res.* 20:810 (1990), Li and Huang, *J. Tissue Cult. Assoc.* 32:129 (1996)). Laine and David, (*Plant Sci.* 69:215 (1990)), however, were able to obtain high frequencies of initiation (up to 59%) in *Pinus caribaea*, suggesting that not all *Pinus* species are recalcitrant. Also, one earlier report described initiation frequencies of 54% in White pine (*Pinus strobus*). Finer et al., *Plant Cell Rep.* 8:203 (1989). However, other workers were not able to duplicate this success. Michler et al., *Plant Sci.* 77:111 (1991). The results in the literature demonstrate the recalcitrance of *Pinus* species, especially Loblolly pine, in regeneration by somatic embryogenesis.

Nevertheless, once this process is understood from the standpoint of developmental genetics, breeders will then have the appropriate tools to monitor, intervene, and improve both the regeneration frequency and the overall quality of tree stock through genetic engineering. For example, both environmental requirements and responsiveness of a developing embryo change as the embryo passes various developmental milestones. Consequently, accurate and timely knowledge of the developmental stage of an embryonic culture would allow the skilled practitioner to beneficially adjust the growth media components and other environmental factors to achieve optimal embryo survival, growth, and maturation. In addition, an understanding of developmentally regulated genes would allow for early selection of advantageous clones and provide tools for developmentally regulated transgenic expression systems.

Currently, a reasonable determination of the precise developmental stage of an embryo requires a practiced, physical familiarity with the morphological appearance of embryos at different stages, which is further complicated by the presence of morphological variations between species. Consequently, visual determination is performed best by experts in the field. Thus, there is a need in the art for a staging method which can be reliably practiced by the ordinary practitioner. The current invention will allow one to stage embryos based on a relational database system profiling gene expression patterns instead of physical morphological differences, thereby permitting one less skilled in the art of visual staging to biologically determine the stages of embryogenesis.

The traditional morphological staging method provides only a crude indication of the underlying biochemical condition or state of an embryo. This level of information is insufficient for refining culture conditions, including media formulations, or for selecting potentially advantageous embryo clones for further development. Thus, there is a need in the art for a more sensitive staging method that precisely defines the physiological age, health, growth requirements, and potential fitness of a particular embryo. The current invention will allow definitive staging significantly beyond that currently practiced in the art, and provides a detailed analysis of the biochemical state and potential fitness of an embryo by comparison to developed relational database profiles.

Visual staging methods depend on morphological markers to assign a numerical stage of 1–9 to an embryo. Nevertheless, it is well accepted that visually undetectable developmental changes occur in an embryo after it reaches stage 9. The current invention is particularly useful in providing means for monitoring and evaluating the developmental state of these older embryos, as genetic responses occur and are detectable up to and through an adult tree's life.

There further exists in the art a need for information regarding the proteins, genes, and gene expression patterns in plant embryo development, as well as a more thorough

understanding of how this information relates to the physiology, developmental potential, and genetic quotient of a plant embryo. The relational database system provides a platform for which to monitor individual gene expression levels during embryo development while directly correlating expression with, for example, environmental conditions, age, and embryo fitness, as well as the protein identification achieved by BLAST searches of publicly available databases (i.e., GenBank) for desirable genes. Accordingly, the present invention therefore provides the additional ability to correlate the direct, global gene expression response within the embryo system to a typically non-expressing gene driven by a stage-specific promoter.

SUMMARY OF THE INVENTION

The present invention addresses these needs by providing in a relational database format nucleic acid and protein sequences that are differentially expressed during various stages of plant embryogenesis. The invention encompasses a set of isolated nucleic acid molecules comprising the DNA sequence of any one of SEQ ID NOS: 1–334 and nucleic acid molecules related or complementary to any one of SEQ ID NOS: 1–334. (See Table I) As such, the invention includes both single-stranded and double-stranded RNA and DNA nucleic acids, including variants thereof. The nucleic acids of the invention can be used as an expression template in the form of DNA arrays, including for example, gene arrays, DNA chips, and dot array Southerns, for which to compare and evaluate expression in test samples. (See Table II) The nucleic acids of the invention can be further used as probes to detect the presence or level of both single-stranded and double-stranded RNA and DNA encoding variants of polypeptides or fragments of polypeptides encompassed by the invention. The nucleic acids of the invention can be further used as promoters for the expression of sense and antisense molecules at specific stages of embryo development. Data acquired through the use of the present invention can in turn be provided to the relational database for further development.

Isolated nucleic acid molecules that hybridize to a denatured, double-stranded DNA comprising the DNA sequence of any one of SEQ ID NOS: 1–334 under conditions of moderate or high stringency are also encompassed by the invention. The invention further encompasses synthetic and naturally-occurring variants of the nucleic acids described in SEQ ID NOS: 1–334, for example, isolated nucleic acid molecules derived by in vitro mutagenesis from SEQ ID NOS: 1–334. In vitro mutagenesis would include numerous techniques known in the art including, but not limited to, site-directed mutagenesis, random mutagenesis, and in vitro nucleic acid synthesis.

The invention also encompasses related molecules (variants) including isolated nucleic acid molecules degenerate from SEQ ID NOS: 1–334 as a result of the genetic code, for example, naturally-occurring or synthetic allelic variants of the genes encoding SEQ ID NOS: 1–334. Such related molecules also encompass both smaller and larger nucleic acids that contain sufficient sequence to support hybridization to any of SEQ ID NOS: 1–334 under conditions of moderate or high stringency. Consequently, recombinant vectors, including those that direct the expression of these nucleic acid molecules and host cells transformed or transfected with these vectors are herein defined as variants and are encompassed by the invention.

Another embodiment of this invention is the production of transgenic vectors and transgenic plants comprising vectors or other nucleic acids comprising any one of SEQ ID NOS: 1–334 and related molecules. Particularly preferred are those capable of expressing polypeptides or peptides encoded by any of SEQ ID NOS: 1–327. In a preferred embodiment, the transgene comprises SEQ ID NO: 327, or a variant thereof.

SEQ ID NO: 327 encodes a protein which corresponds to a novel Loblolly pine homolog of the plant Major Intrinsic Protein (MIP) family. MIPs comprise a large family of related proteins that function as membrane channels for the transport of water and possibly ions across cellular membranes. Henceforth, the encoded protein of SEQ ID NO: 327 may be referred to as Loblolly MIP. Variants, including naturally-occurring and artifactually-programmed allelic variants, vectors, and other nucleic acids which hybridize to SEQ ID NO: 327 under conditions of moderate or high stringency are encompassed by the invention. Also encompassed are plant cells, seeds, embryos and trees, transgenic for loblolly pine MIP, and variants thereof.

The invention also encompasses isolated polypeptides, or fragments thereof, encoded by any one of the nucleic acid molecules of SEQ ID NOS: 1–327, including variants thereof. The invention further encompasses the use of these peptide sequences as markers for staging, monitoring, and selecting embryos and embryo cultures. The invention also encompasses methods for the production of these polypeptides or fragments thereof including culturing a host cell under conditions promoting expression and recovering the polypeptide or peptide from the culture medium. In particular, the expression of polypeptides or peptides encoded by SEQ ID NOS: 1–327 in viral vectors, bacteria, yeast, plant, and animal cells is encompassed by the invention. Isolated polyclonal or monoclonal antibodies that bind to peptides encoded by SEQ ID NOS: 1–327 are also encompassed by the invention.

Further encompassed by this invention are methods for using the nucleic acid molecules of any one of SEQ ID NOS: 1–327 to obtain full length cDNA and genomic sequences of the corresponding genes, including cognate, homologous, or otherwise related genetic sequences, which hybridize to any of SEQ ID NOS: 1–327 under conditions of moderate or high stringency. Also provided by this invention are oligonucleotides derived from any one of SEQ ID NOS: 1–334 that can be used as probes and/or as primers in PCR, RT-PCR, and other assays to detect the presence or level of the nucleic acids of SEQ ID NOS: 1–334 and related molecules.

The primers and other probes of the invention may be used to monitor and characterize the development of plant embryos, in particular, pine tree embryos. Characterization of embryonic gene expression provides means for correlating gene expression with current and potential plant phenotypes. Consequently, the present invention encompasses means for monitoring and adjusting growth conditions (see FIG. **6**), as well as means for selecting genetically superior embryonic clones for further propagation and expansion (see FIG. **8**). Thus, the present invention encompasses the use of DNA or RNA probes derived from the nucleic acid molecules of SEQ ID NOS: 1–334 in any form, e.g., in DNA arrays, and antibodies raised against polypeptides or peptide fragments encoded by SEQ ID NOS: 1–327, to determine relative or absolute levels of expression of the genes or proteins encoded by SEQ ID NOS: 1–327. In addition, these nucleic acid and antibody probes may be used for staging, monitoring, characterizing, or selecting plant embryos or embryo cultures, particularly pine tree embryos.

The relational database of the present invention allows expression information pertaining to embryo stages to be viewed as sequence data generated in accordance with the present invention. The invention includes a database for storing a plurality of sequence records for which to correlate embryo stages to sequence records. The method further involves providing an interface which allows a user to select one or more expression categories contained within the database.

The relational database is designed to include separate parts or cells for information storage. One cell or part may contain a gene expression database which contains nucleic acid molecules of SEQ ID NOS: 1–327. Other cells or parts may contain descriptive information pertaining to each nucleic acid molecules of SEQ ID NOS: 1–327, additional sequence data related to the gene expression database, protein encoded by nucleic acids disclosed herein, similarity values to known proteins of other systems, and to conditions under which expression data was obtained.

The database system described in the present invention will allow identification or selection of particular genes of interest for further use with DNA arrays. Identification or selection of particular genes may include, for example, those related to patterns of expression, those identified with homology to known genes from other studies, and those sequences considered novel.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** depicts differential display of loblolly pine zygotic and somatic embryos at different stages of development.

FIG. **2** displays embryo gene expression observed by high-density array Southern hybridization.

FIG. **3** provides a general schematic for gene regulation studies arising from the cDNA cloning of genes expressed in embryos.

FIG. **4** depicts graphical representation of hybridization of 'dehydrin' and LPZ216 cDNA probes to total RNA isolated from zygotic embryos of loblolly pine.

FIG. **5** displays ABA concentration of loblolly pine embryos.

FIG. **6** shows schematic of gene study for improved somatic embryogenesis.

FIG. **7** shows detection of gene expression by high-density array Southern hybridization for loblolly pine genotype 333 after 12 weeks on two maturation media.

FIG. **8** depicts the application of embryogenic gene expression studies.

FIG. **9** displays slot blots and expression levels for three embryogenesis-related genes.

FIG. **10** depicts clone LPS-097 sequence (SEQ ID NO: 339) (LP2-3 differential display fragment.)

FIG. **11** displays a northern blot for the LP2-3 gene during stages 1–3.

FIG. **12** displays a slot blot of total RNA from somatic embryo tissue probed with an LP2-3-specific probe. Panel A depicts an image of the slot blot and panel B depicts quantitation of the image.

FIG. **13** displays a slot blot of total RNA from zygotic embryo tissue probed with an LP2-3-specific probe. Panel A depicts an image of the slot blot and panel B depicts quantitation of the image.

FIG. **14** depicts the quantified expression of early zygotic embryos compared to early somatic embryos. Panel A depicts an image of the slot blot and panel B depicts quantitation of the image.

DETAILED DESCRIPTION OF THE INVENTION

The three hundred and twenty-seven differentially expressed cDNAs isolated from plant specimens of known developmental ages are disclosed in SEQ ID NOS: 1–327. The seven stage-specific promoters isolated from plant specimens are disclosed in SEQ ID NOS: 328–334. The discovery of these cDNAs and promoters enables the design, isolation, and construction of related nucleic acids, proteins, antigens, antibodies other heterologous genes. Both the cDNAs and promoters facilitate the staging, characterization, and manipulation of plant embyrogenesis, in particular, conifer embryogenesis. These molecules, and related nucleic acids, peptides, proteins, antigens, and antibodies are particularly useful when compiled into a relational database for the monitoring, design, selection, and cultivation of improved crop plants.

The cDNAs of SEQ ID NOS: 1–327, in addition to the promoters of SEQ ID NOS: 328–334, were originally derived from *Pinus taeda* embryos, commonly known as the Loblolly Pine. Nevertheless, it is understood that the invention is applicable to and encompasses all plants, including all dicotyledonous plants, including all conifers, including all species of *Pinus, Picea*, and *Pseudotsuga*. Exemplary conifers may include *Picea abies*, and *Psedotsuga menziesii*, and *Pinus taeda*.

Nucleic Acid Molecules

In a particular embodiment, the invention relates to certain isolated nucleotide sequences including those that are substantially free from contaminating endogenous material. The terms "nucleic acid" or "nucleic acid molecule" refer to a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, and unless otherwise limited, would encompass known analogs of natural nucleotides that can function in a similar manner as naturally occurring nucleotides. A "nucleotide sequence" also refers to a polynucleotide molecule or oligonucleotide molecule in the form of a separate fragment or as a component of a larger nucleic acid. The nucleotide sequence or molecule may also be referred to as a "nucleotide probe." The nucleic acid molecules of the invention are derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequence by standard biochemical methods. Examples of such methods, including methods for PCR protocols that may be used herein, are disclosed in Sambrook et al., *Molecular Cloning: A Laboratory Manual,* 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1989), *Current Protocols in Molecular Biology* edited by F. A. Ausubel et al., John Wiley and Sons, Inc. (1987), and Innis, M. et al., eds., *PCR Protocols: A Guide to Methods and Applications*, Academic Press (1990), each of which are herein incorporated by reference in their entirety.

As used herein a "nucleotide probe" is defined as an oligonucleotide capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, through complementary base pairing, or through hydrogen bond formation. As described above, the oligonucleotide probe may include natural (ie. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, bases in a oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, so long as it does

not prevent hybridization. Thus, oligonucleotide probes may have constituent bases joined by peptide bonds rather than phosphodiester linkages.

A "target nucleic acid" herein refers to a nucleic acid to which the nucleotide probe or molecule can specifically hybridize. The probe is designed to determine the presence or absence of the target nucleic acid, and the amount of target nucleic acid. The target nucleic acid has a sequence that is complementary to the nucleic acid sequence of the corresponding probe directed to the target. As recognized by one of skill in the art, the probe may also contain additional nucleic acids or other moieties, such as labels, which may not specifically hybridize to the target. The term target nucleic acid may refer to the specific nucleotide sequence of a larger nucleic acid to which the probe is directed or to the overall sequence (e.g., gene or mRNA) whose expression level it is desired to detect. One skilled in the art will recognize the full utility under various conditions.

As described herein, the nucleic acid molecules of the invention include DNA in both single-stranded and double-stranded form, as well as the RNA complement thereof. DNA includes, for example, cDNA, genomic DNA, chemically synthesized DNA, DNA amplified by PCR, and combinations thereof. Genomic DNA, including translated, non-translated and control regions, may be isolated by conventional techniques, e.g., using any one of the cDNAs of SEQ ID NO: 1 through SEQ ID NO: 327, or suitable fragments thereof, as a probe, to identify a piece of genomic DNA which can then be cloned using methods commonly known in the art. In general, nucleic acid molecules within the scope of the invention include sequences that hybridize to sequences of SEQ ID NOS: 1–334 under hybridization and wash conditions of 5°, 10°, 15°, 20°, 25°, or 30° below the melting temperature of the DNA duplex of sequences of SEQ ID NOS: 1–334, including any range of conditions subsumed within these ranges.

DNA Arrays

In a further embodiment, DNA arrays are used to identify hybridizing sequences from test samples. The term "DNA array" refers to "gene arrays," "DNA chips," "dot array Southerns," etc. One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The DNA array will typically include one or a multiplicity of nucleic acid molecules derived from SEQ ID NO: 1 through SEQ ID NO: 327 that specifically hybridize to the nucleic acid expression of which is to be detected. In addition, the array may include one or more control probes to monitor the expression system. Control probes refer to known expression products present at each stage of expression, e.g., ribosomal gene products or the transcripts of other housekeeping genes. The organization of the DNA array will be known to facilitate interpretation of results. Examples in the art describing the uses and composition of DNA arrays can be found in U.S. Pat. Nos. 5,700,637, 5,837,832, 5,843,655, 5,874,219, 6,040,138, 6,045,996, and are incorporated by reference.

Molecules that Hybridize to Identified Sequences

Thus, in a particular embodiment, this invention provides an isolated nucleic acid molecule selected from the group consisting of:

(1) a DNA sequence comprising any one of the sequences presented in SEQ ID NO: 1 through SEQ ID NO: 334;

(2) an isolated nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of (a) under conditions of moderate stringency; and

(3) an isolated nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of (a) under conditions of high stringency.

As used herein, stringency conditions in nucleic acid hybridizations can be readily determined by those having ordinary skill in the art based on, for example, the length and composition of the nucleic acid. In one embodiment, moderate stringency is herein defined as a nucleic acid having 10, 11, 12, 13, 14, 15, 16, or 17, contiguous nucleotides identical to any of the sequences of SEQ ID NOS: 1–334, or a complement thereof. Similarly, high stringency is hereby defined as a nucleic acid having 18, 19, 20, 21, 22, or more contiguous identical nucleotides, or a longer nucleic acid having at least 80, 85, 90, 95, or 99 percent identity with any of the sequences of SEQ ID NOS: 1–334; for sequences of at least 50, 100, 150, 200, or 250 nucleotides, high stringency may comprise an overall identity of at least 60, 65, 70 or 75 percent.

Generally, nucleic acid hybridization simply involves providing a denatured nucleotide molecule or probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. The nucleic acids that do not substantially form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is further generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under lower stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

As used herein, the percent identity between an amino acid sequence encoded by any of SEQ ID NOS: 1–334 and a potential hybridizing variant can be determined, for example, by comparing sequence information using the GAP computer program, version 6.0 described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) and available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program utilizes the alignment method of Needleman and Wunsch (*J. Mol. Biol.* 48:443, 1970), as revised by Smith and Waterman (*Adv. Appl. Math* 2:482, 1981). The preferred default parameters for the GAP program include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) for nucleotides, and the weighted comparison matrix of Gribskov and Burgess (*Nucl. Acids Res.* 14:6745, 1986), as described by Schwartz and Dayhoff (eds., *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, pp. 353–358, 1979); (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

Alternatively, basic protocols for empirically determining hybridization stringency are set forth in section 2.10 of *Current Protocols in Molecular Biology* edited by F. A. Ausubel et al., John Wiley and Sons, Inc. (1987). Stringency conditions can be determined readily by the skilled artisan. An example of moderate stringency hybridization conditions would be hybridization in 5×SSC, 5× Denhardt's Solution, 50% (w/v) formamide, and 1% SDS at 42° C. with

washing conditions of 0.2×SSC and 0.1% SDS at 42° C. An example of high stringency conditions can be defined as hybridization conditions as above, and with washing at approximately 68° C., in 0.1×SSC, and 0.1% SDS. The skilled artisan will recognize that the temperature and wash solution salt concentration can be adjusted as necessary according to factors such as the length of the probe.

Due to the degeneracy of the genetic code wherein more than one codon can encode the same amino acid, multiple DNA sequences can code for the same polypeptide. Such variant DNA sequences can result from genetic drift or artificial manipulation (e.g., occurring during PCR amplification or as the product of deliberate mutagenesis of a native sequence). The present invention thus encompasses any nucleic acid capable of encoding a protein derived from SEQ ID NOS: 1–327, or variants thereof.

Deliberate mutagenesis of a native sequence can be carried out using numerous techniques well known in the art. For example, oligonucleotide-directed site-specific mutagenesis procedures can be employed, particularly where it is desired to mutate a gene such that predetermined restriction nucleotides or codons are altered by substitution, deletion or insertion. Exemplary methods of making such alterations are disclosed by Walder et al. (*Gene* 42:133, 1986); Bauer et al. (Gene 37:73, 1985); Craik (*BioTechniques*, Jan. 12–19, 1985); Smith et al. (*Genetic Engineering: Principles and Methods*, Plenum Press, 1981); Kunkel (*Proc. Natl. Acad. Sci. USA* 82:488, 1985); Kunkel et al. (*Methods in Enzymol.* 154:367, 1987); and U.S. Pat. Nos. 4,518,584 and 4,737,462, all of which are incorporated by reference.

Thus, the invention further provides an isolated nucleic acid molecule selected from the group comprising of (1), (2), and (3) above and further consisting of:

(4) an isolated nucleic acid molecule degenerate from SEQ ID NOS: 1–334 as a result of the genetic code; and

(5) an isolated nucleic acid molecule selected from the group consisting of an allelic variants and species homologs of SEQ ID NOS: 1–334.

Obtaining Full Length cDNAs

The cDNAs isolated and cloned through the differential display procedure will often only represent a partial sequence (generally the 3' end) of the mRNA from which it was derived due to the nature of the arbitrary primer used in the differential display PCR reaction. Consequently, the cDNA sequences of SEQ ID NOS: 1–327 provide powerful tools for obtaining the sequences of full-length cDNAs. This can be accomplished by using a partial cDNA as a probe to identify and isolate the full length cDNA from a population of full length cDNAs or from a full length cDNA library. As is well known in the art, similar procedures can be used to identify corresponding genomic DNA sequences.

Alternatively, one can obtain the 5' sequence of a partial cDNA by performing Rapid Amplification of cDNA Ends (RACE) procedures such as those disclosed in Frohman, *Methods in Enzymology,* 218:340–356 (1993) and Bertling et al., *PCR Methods and Applications* 3:95–99 (1993) which are hereby incorporated by reference. For example, Clonetech Laboratories, Inc. (Palo Alto, Calif.) offers a SMART™ cDNA product line that allows one to generate high quality full length cDNAs and cDNA libraries. SMART™ technology can also be used to perform RACE. One skilled in the art will readily recognize that there are other equivalent products and procedures for obtaining full length cDNAs. Full length cDNAs may be sequenced and their sequences compared to sequences in public databases to assess their identities and/or homologies to other known sequences.

Cloned full length cDNAs can be used in the construction of expression vectors for the production and purification of pine tree polypeptides which contain the pine tree peptides encoded by the cDNAs of any one of SEQ ID NOS: 1–327.

Oligonucleotide Primers for PCR Assays

In another embodiment, the present invention encompasses oligonucleotide fragments derived from any one of SEQ ID NO: 1 through SEQ ID NO: 327 or from the reverse complement sequence of any one of SEQ ID NO: 1 through SEQ ID NO: 327. Such oligonucleotides would be useful as primers in the performance of RT-PCR assays to detect, or even quantify, pine embryo stage-specific transcripts. Such oligonucleotide primers will generally comprise from 10 to 25 nucleotides substantially complementary to the ends of the target sequence and may contain additional non-complementary nucleotides, for example, nucleotides that generate a restriction endonuclease site or cloning junction. Programs useful in selecting PCR primers may be used to design the oligonucleotides of this invention, but use of such programs is not necessary. By way of example, the Wisconsin Package™ software available from the Genetic Computer Group (Madison, Wis.) includes a program called Prime that can aid in selecting primers from a given template sequence. Protocols for the design and optimization of PCR reactions are commonly known in the art and are described in Saiki et al., *Science* 239:487 (1988); *Recombinant DNA Methodology*, Wu et al., eds., Academic Press, Inc., San Diego (1989), pp. 189–196; and PCR Protocols: *A Guide to Methods and Applications*, Innis et al., eds., Academic Press, Inc. (1990).

Antisense Nucleic Acid Molecules

Other useful fragments of the nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of DNA from any one of SEQ ID NO: 1 through SEQ ID NO: 327. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to about 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*Bio/Techniques* 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes or other nucleic acid complexes inimical to efficient production of gene products. The antisense oligonucleotides thus may be used to block expression of proteins or the function of RNA. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable in vivo (i.e., capable of resisting enzymatic degradation) but retain sufficient sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10448, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as

poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides. Such modifications may modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, lipofection, $CaPO^4$-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus or adenovirus.

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. In one embodiment, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Polypeptides Encoded by Differentially-Expressed cDNAs

The cDNAs of SEQ ID NOS: 1–327 can be translated into amino acid sequences potentially corresponding to portions of developmentally-regulated plant proteins. These amino acid sequences can be identified from sequences listed in Table I, below. The cDNAs encoding these predicted polypeptides are grouped into early, middle, and late transcripts according to the staged embryo population from which they were derived.

(See Table I)

Although the term "peptide" is generally understood to reference synthetic sequences, or fragments of larger proteins, and includes short amino acid sequences of between 2 and 10 amino acids, whereas "polypeptide" refers to larger sequences and full-length proteins, the terms are used interchangeably herein to indicate that the invention applies to peptides and polypeptides of any length and variants thereof. Moreover, the discovery of presumptive open reading frames in SEQ ID NOS: 1–327, and the ability to isolate additional cDNA sequence, enables the construction of expression vectors comprising nucleic acid sequences encoding those polypeptides. The cDNAs of the invention also enable cells transfected or transformed with expression vectors driving the expression of the encoded polypeptides and antibodies reactive with the polypeptides.

In one embodiment, the invention provides for isolated polypeptides, preferably, pine tree polypeptides. As used herein, the term "polypeptides" refers to a genus of polypeptide or peptide fragments that encompass the amino acid sequences identified from Table I, as well as smaller fragments. Consequently, the invention encompasses any polypeptide fragment comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 contiguous amino acids encoded by the cDNAs of any of SEQ ID NOS: 1–327, or comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 contiguous amino acids of any of amino acid sequence derived from Table I.

Alternatively, a polypeptide may be defined in terms of its antigenic relatedness to any peptide encoded by SEQ ID NOS: 1–327. Thus, in one embodiment, a polypeptide within the scope of the invention is defined as an amino acid sequence comprising a linear or 3-dimensional epitope shared with any peptide encoded by the cDNAs of SEQ ID NOS: 1–327. Alternatively, a polypeptide within the scope of the invention is recognized by an antibody that specifically recognizes any peptide encoded by SEQ ID NOS: 1–327. Antibodies are defined to be specifically binding if they bind pine tree polypeptides with a K_a of greater than or equal to about 10^7 M^{-1}, and preferably greater than or equal to 10^8 M^{-1}.

A polypeptide "variant" as referred to herein means a polypeptide substantially homologous to a native polypeptide, but which has an amino acid sequence different from that encoded by any of SEQ ID NOS: 1–327 because of one or more deletions, insertions or substitutions. The variant amino acid sequence preferably is at least 80% identical to a native polypeptide amino acid sequence, preferably at least 90%, more preferably, at least 95% identical over at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21–25, or 26–30 contiguous amino acids. The percent identity between an amino acid sequence encoded by any of SEQ ID NOS: 1–327 and a potential variant can be determined manually, or, for example, by comparing sequence information using the GAP computer program, version 6.0 described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) and available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program, described above, utilizes the alignment method of Needleman and Wunsch (*J. Mol. Biol.* 48:443, 1970), as revised by Smith and Waterman (*Adv. Appl. Math* 2:482, 1981).

Variants can comprise conservatively substituted sequences, meaning that a given amino acid residue is replaced by a residue having similar physiochemical characteristics. Examples of conservative substitutions include substitution of one aliphatic residue for another, such as lie, Val, Leu, or Ala for one another, or substitutions of one polar residue for another, such as between Lys and Arg; Glu and Asp; or Gin and Asn. See Zubay, Biochemistry, Addison-Wesley Pub. Co., (1983) incorporated by reference in its entirety. The effects of such substitutions can be calculated using substitution score matrices such a PAM-120, PAM-200, and PAM-250 as discussed in Altschul, (*J. Mol. Biol.* 219:555–65, 1991). Other such conservative substitutions, for example, substitutions of entire regions having similar hydrophobicity characteristics, are well known.

Naturally-occurring peptide variants are also encompassed by the invention. Examples of such variants are proteins that result from alternate mRNA splicing events or from proteolytic cleavage of the polypeptides of Table I. Variations attributable to proteolysis include, for example, differences in the N- or C-termini upon expression in different types of host cells, due to proteolytic removal of one or more terminal amino acids from the polypeptides encoded by the sequences of Table I (generally from 1–5 terminal amino acids).

As stated above, the invention provides recombinant and non-recombinant, isolated and purified polypeptides, preferably pine tree polypeptides. Variants and derivatives of native polypeptides can be obtained by isolating naturally-occurring variants, or the nucleotide sequence of variants, of other plant lines or species, or by artificially programming mutations of nucleotide sequences coding for native pine tree polypeptides. Alterations of the native amino acid sequence can be accomplished by any of a number of

conventional methods. Mutations can be introduced at particular loci by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments of the native sequence. Following ligation, the resulting reconstructed sequence encodes an analog having the desired amino acid insertion, substitution, or deletion. Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered gene wherein predetermined codons can be altered by substitution, deletion or insertion. Exemplary methods of making such alterations are discussed supra.

The following sections are examples of the various expression vectors, host cells, and protein purification methods that are known in the art. These examples are provided merely as illustrative and should not be construed as the only means to express and purify the polypeptides and polypeptide variants of the invention.

Expression Vectors and Purified Proteins

Recombinant expression vectors containing a nucleic acid sequence encoding the polypeptides of the invention can be prepared using well known methods. In one embodiment, the expression vectors include a cDNA sequence encoding the polypeptide operably linked to suitable transcriptional or translational regulatory nucleotide sequences, such as those derived from a mammalian, microbial, viral, or insect gene. Examples of regulatory sequences include transcriptional promoters, operators, or enhancers, mRNA ribosomal binding sites, and appropriate sequences which control transcription and translation initiation and termination. Nucleotide sequences are "operably linked" when the regulatory sequence functionally relates to the cDNA sequence of the invention. Thus, a promoter nucleotide sequence is operably linked to a cDNA sequence if the promoter nucleotide sequence controls the transcription of the cDNA sequence. The ability to replicate in the desired host cells, usually conferred by an origin of replication, and a selection gene by which transformants are identified can additionally be incorporated into the expression vector.

In addition, sequences encoding appropriate signal peptides that are not naturally associated with the polypeptides of the invention can be incorporated into expression vectors. For example, a DNA sequence for a signal peptide (secretory leader) can be fused in-frame to the pine tree nucleotide sequence so that the polypeptides of the invention is initially translated as a fusion protein comprising the signal peptide. A signal peptide that is functional in the intended host cells enhances extracellular secretion of the expressed polypeptide. The signal peptide can be cleaved from the polypeptide upon secretion from the cell.

Fusions of additional peptide sequences at the amino and carboxyl terminal ends of the polypeptides of the invention can be used to enhance expression of the polypeptides or aid in the purification of the protein. Such peptides include, for example, poly-His or the antigenic identification peptides described in U.S. Pat. No. 5,011,912 and in Hopp et al., (*Bio/Technology* 6:1204, 1988).

Suitable host cells for expression of polypeptides of the invention include prokaryotes, yeast or higher eukaryotic cells. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described, for example, in Pouwels et al., *Cloning Vectors: A Laboratory Manual*, Elsevier, N.Y., (1985). Cell-free translation systems could also be employed to the disclosed polypeptides using RNAs derived from DNA constructs disclosed herein.

Prokaryotic Expression Systems

Prokaryotes include gram negative or gram positive organisms, for example, *E. coli* or *Bacilli*. Suitable prokaryotic host cells for transformation include, for example, *E. coli, Bacillus subtilis, Salmonella typhimurium*, and various other species within the genera *Pseudomonas, Streptomyces*, and *Staphylococcus*. In a prokaryotic host cell, such as *E. coli*, the disclosed polypeptides can include an N-terminal methionine residue to facilitate expression of the recombinant polypeptide in the prokaryotic host cell. The N-terminal methionine can be cleaved from the expressed recombinant polypeptide.

Expression vectors for use in prokaryotic host cells generally comprise one or more phenotypic selectable marker genes. A phenotypic selectable marker gene is, for example, a gene encoding a protein that confers antibiotic resistance or that supplies an autotrophic requirement. Examples of useful expression vectors for prokaryotic host cells include those derived from commercially available plasmids such as the cloning vector pBR322 (ATCC 37017). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. To construct an expression vector using pBR322, an appropriate promoter and a DNA sequence encoding one or more of the polypeptides of the invention are inserted into the pBR322 vector. Other commercially available vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM-1 (Promega Biotec, Madison, Wis., USA). Other commercially available vectors include those that are specifically designed for the expression of proteins; these would include pMAL-p2 and pMAL-c2 vectors that are used for the expression of proteins fused to maltose binding protein (New England Biolabs, Beverly, Mass., USA).

Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include β-lactamase (penicillinase), lactose promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EP-A-36776), and tac promoter (Maniatis, *MoLecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982). A particularly useful prokaryotic host cell expression system employs a phage λ P_L promoter and a cI857ts thermolabile repressor sequence. Plasmid vectors available from the American Type Culture Collection ("ATCC"), which incorporate derivatives of the PL promoter, include plasmid pHUB2 (resident in *E. coli* strain JMB9 (ATCC 37092)) and pPLc28 (resident in *E. coli* RR1 (ATCC 53082)).

DNA encoding one or more of the polypeptides of the invention may be cloned in-frame into the multiple cloning site of an ordinary bacterial expression vector. Ideally the vector would contain an inducible promoter upstream of the cloning site, such that addition of an inducer leads to high-level production of the recombinant protein at a time of the investigator's choosing. For some proteins, expression levels may be boosted by incorporation of codons encoding a fusion partner (such as hexahistidine) between the promoter and the gene of interest. The resulting "expression plasmid" may be propagated in a variety of strains of *E. coli*.

For expression of the recombinant protein, the bacterial cells are propagated in growth medium until reaching a pre-determined optical density. Expression of the recombinant protein is then induced, e.g., by addition of IPTG (isopropyl-b-D-thiogalactopyranoside), which activates expression of proteins from plasmids containing a lac operator/promoter. After induction (typically for 1–4 hours), the

cells are harvested by pelleting in a centrifuge, e.g., at 5,000×G for 20 minutes at 4° C.

For recovery of the expressed protein, the pelleted cells may be resuspended in ten volumes of 50 mM Tris-HCl (pH 8)/1 M NaCl and then passed two or three times through a French press. Most highly expressed recombinant proteins forms insoluble aggregates known as inclusion bodies. Inclusion bodies can be purified away from the soluble proteins by pelleting in a centrifuge at 5,000×G for 20 minutes, 4° C. The inclusion body pellet is washed with 50 mM Tris-HCl (pH 8)/1% Triton X-100 and then dissolved in 50 mM Tris-HCl (pH 8)/8 M urea/0.1 M DTT. Any material that cannot be dissolved in 50 mM Tris-HCl (pH 8)/8 M urea/0.1 M DTT may be removed by centrifugation (10, 000×G for 20 minutes, 20° C.). The protein of interest will, in most cases, be the most abundant protein in the resulting clarified supernatant. This protein may be "refolded" into the active conformation by dialysis against 50 mM Tris-HCl (pH 8)/5 mM $CaCl_2$/5 mM $Zn(OAc)_2$/1 mM GSSG/0.1 mM GSH. After refolding, purification can be carried out by a variety of chromatographic methods such as ion exchange or gel filtration. In some protocols, initial purification may be carried out before refolding. As an example, hexahistidine-tagged fusion proteins may be partially purified on immobilized Nickel.

While the preceding purification and refolding procedure assumes that the protein is best recovered from inclusion bodies, those skilled in the art of protein purification will appreciate that many recombinant proteins are best purified out of the soluble fraction of cell lysates. In these cases, refolding is often not required, and purification by standard chromatographic methods can be carried out directly.

Yeast Expression Systems

Polypeptides of the invention can also be expressed in yeast host cells, preferably from the *Saccharomyces* genus (e.g., *S. cerevisiae*). Other genera of yeast, such as *Pichia* or *Kluyveromyces* (e.g. *K. lactis*), can also be employed. Yeast vectors will often contain an origin of replication sequence from a 2μ yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, sequences for transcription termination, and a selectable marker gene. Suitable promoter sequences for yeast vectors include, among others, promoters for metallothionine, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980), or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Other suitable vectors and promoters for use in yeast expression are further described in Hitzeman, EPA-73,657 or in Fleer et. al., *Gene,* 107:285–195 (1991); and van den Berg et. al., *Bio/Technology,* 8:135–139 (1990). Another alternative is the glucose-repressible ADH2 promoter described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). Shuttle vectors replicable in both yeast and *E. coli* can be constructed by inserting DNA sequences from pBR322 for selection and replication in *E. coli* (Amp^r gene and origin of replication) into the above-described yeast vectors.

The yeast α-factor leader sequence can be employed to direct secretion of one or more of the disclosed polypeptides. The α-factor leader sequence is often inserted between the promoter sequence and the structural gene sequence. See, e.g., Kurjan et al., *Cell* 30:933, 1982; Bitter et al., *Proc. Natl. Acad. Sci. USA* 81:5330, 1984; U.S. Pat. No. 4,546,082; and EP 324,274. Other leader sequences suitable for facilitating secretion of recombinant polypeptides from yeast hosts are known to those of skill in the art. A leader sequence can be modified near its 3' end to contain one or more restriction sites. This will facilitate fusion of the leader sequence to the structural gene.

Yeast transformation protocols are known to those of skill in the art. One such protocol is described by Hinnen et al., *Proc. Natl. Acad. Sci. USA* 75:1929, 1978. The Hinnen et al. protocol selects for Trp+ transformants in a selective medium, wherein the selective medium consists of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 μg/ml adenine, and 20 μg/ml uracil.

Yeast host cells transformed by vectors containing ADH2 promoter sequence can be grown for inducing expression in a "rich" medium. An example of a rich medium is one consisting of 1% yeast extract, 2% peptone, and 1% glucose supplemented with 80 μg/ml adenine and 80 μg/ml uracil. Derepression of the ADH2 promoter occurs when glucose is exhausted from the medium.

Mammalian Expression Systems

Mammalian or insect host cell culture systems could also be employed to express recombinant polypeptides of the invention. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, *Bio/Technology* 6:47 (1988). Established cell lines of mammalian origin also can be employed. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., *Cell* 23:175, 1981), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, HeLa cells, and BHK (ATCC CRL 10) cell lines, and the CV-1/EBNA-1 cell line (ATCC CRL 10478) derived from the African green monkey kidney cell line CVI (ATCC CCL 70) as described by McMahan et al. (*EMBO J.* 10: 2821, 1991).

Established methods for introducing DNA into mammalian cells have been described (Kaufman, R. J., *Large Scale Mammalian Cell Culture,* 1990, pp. 15–69). Additional protocols using commercially available reagents, such as Lipofectamine (Gibco/BRL) or Lipofectamine-Plus, can be used to transfect cells (Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413–7417, 1987). In addition, electroporation can be used to transfect mammalian cells using conventional procedures, such as those in Sambrook et al. Molecular Cloning: A Laboratory Manual, 2 ed. Vol. 1–3, Cold Spring Harbor Laboratory Press, 1989). Selection of stable transformants can be performed using resistance to cytotoxic drugs as a selection method. Kaufman et al., *Meth. in Enzymology* 185:487–511, 1990, describes several selection schemes, such as dihydrofolate reductase (DHFR) resistance. A suitable host strain for DHFR selection can be CHO strain DX-B11, which is deficient in DHFR (Urlaub and Chasin, *Proc. Natl. Acad. Sci.* USA 77:4216–4220, 1980). A plasmid expressing the DHFR cDNA can be introduced into strain DX-B11, and only cells that contain the plasmid can grow in the appropriate selective media. Other examples of selectable markers that can be incorporated into an expression vector include cDNAs conferring resistance to antibiotcs, such as G418 and hygromycin B. Cells harboring the vector can be selected on the basis of resistance to these compounds.

Transcriptional and translational control sequences for mammalian host cell expression vectors can be excised from viral genomes. Commonly used promoter sequences and

enhancer sequences are derived from polyoma virus, adenovirus 2, simian virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and later promoter, enhancer, splice, and polyadenylation sites can be used to provide other genetic elements for expression of a structural gene sequence in a mammalian host cell. Viral early and late promoters are particularly useful because both are easily obtained from a viral genome as a fragment, which can also contain a viral origin of replication (Fiers et al., *Nature* 273:113, 1978; Kaufman, *Meth. in Enzymology,* 1990). Smaller or larger SV40 fragments can also be used, provided the approximately 250 bp sequence extending from the Hind III site toward the Bgl I site located in the SV40 viral origin of replication site is included.

Additional control sequences shown to improve expression of heterologous genes from mammalian expression vectors include such elements as the expression augmenting sequence element (EASE) derived from CHO cells (Morris et al., *Animal Cell Technology,* 1997, pp. 529–534) and the tripartite leader (TPL) and VA gene RNAs from Adenovirus 2 (Gingeras et al., *J. Biol. Chem.* 257:13475–13491, 1982). The internal ribosome entry site (IRES) sequences of viral origin allows dicistronic mRNAs to be translated efficiently (Oh and Sarnow, *Current Opinion in Genetics and Development* 3:295–300, 1993; Ramesh et al., *Nucleic Acids Research* 24:2697–2700, 1996). Expression of a heterologous cDNA as part of a dicistronic mRNA followed by the gene for a selectable marker (eg. DHFR) has been shown to improve transfectability of the host and expression of the heterologous cDNA (Kaufman, *Meth. in Enzymology,* 1990). Exemplary expression vectors that employ dicistronic mRNAs are pTR-DC/GFP described by Mosser et al., *Biotechniques* 22:150–161, 1997, and p2A5I described by Morris et al., *Animal Cell Technology,* 1997, pp. 529–534.

A useful high expression vector, pCAVNOT, has been described by Mosley et al., Cell 59:335–348, 1989. Other expression vectors for use in mammalian host cells can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280, 1983). A useful system for stable high level expression of mammalian cDNAs in C127 murine mammary epithelial cells can be constructed substantially as described by Cosman et al. (*Mol. Immunol.* 23:935, 1986). A useful high expression vector, PMLSV N1/N4, described by Cosman et al., *Nature* 312:768, 1984, has been deposited as ATCC 39890. Additional useful mammalian expression vectors are described in EP-A-0367566, and in U.S. patent application Ser. No. 07/701,415, filed May 16, 1991, incorporated by reference herein. The vectors can be derived from retroviruses. In place of the native signal sequence, a heterologous signal sequence can be added, such as the signal sequence for IL-7 described in U.S. Pat. No. 4,965,195; the signal sequence for IL-2 receptor described in Cosman et al., Nature 312:768 (1984); the IL-4 signal peptide described in EP 367,566; the type I IL-1 receptor signal peptide described in U.S. Pat. No. 4,968,607; and the type H IL-1 receptor signal peptide described in EP 460,846.

The polypeptides of the invention and the nucleic acid molecules encoding them can also be used as reagents to identify (a) proteins that the disclosed polypeptides or their constituent proteins regulate, and (b) other proteins with which it might interact. The disclosed polypeptides can be coupled to a recombinant protein, to an affinity matrix, or by using them as a bait in the yeast two-hybrid system. The use of the yeast two-hybrid system developed by Stanley Fields and coworkers is well known in the art and described in Golemis, E., et al Section 20.1 in: Current Protocols in Molecular Biology, ed. Ausubel, F. M., et al., John Wiley & Sons, NY, 1997 and in *The Yeast Two-Hybrid System.*, ed. P. L. Bartel and S. Fields, Oxford University Press, 1997.

Antibodies and Peptide Binding Proteins

Purified polypeptides of the invention can be used to generate antibodies that bind to one or more epitopes of the disclosed polypeptide. Such anti-polypeptide antibodies includes polyclonal antibodies, monoclonal antibodies, fragments thereof such as F(ab')2, and Fab fragments, as well as any recombinantly produced binding partners. Antibodies are defined to be specifically binding if they bind pine tree polypeptides with a K_a of greater than or equal to about 10^7 M^{-1}. Affinities of binding partners or antibodies can be readily determined using conventional techniques, for example, those described by Scatchard et al., *Ann. N.Y. Acad. Sci.,* 51:660 (1949).

Polyclonal antibodies can be readily generated from a variety of sources, for example, horses, cows, goats, sheep, dogs, chickens, rabbits, mice, hamsters, guinea pigs, or rats, using procedures that are well-known in the art, for example, as described for example, in U.S. Pat. No. 5,585,100, incorporated by reference herein. In general, a composition comprising at least one of the polypeptides of the invention is administered to the host animal, typically through intraperitoneal or subcutaneous injection. In the case where a peptide is used as the immunogen, it is preferable to conjugated it to a suitable carrier molecule, such as a T-dependent antigen (Bovine Serum Albumin, cholera toxin, and the like). The immunogenicity of the disclosed polypeptides can also be enhanced through the use of an adjuvant, for example, Freund's complete or incomplete adjuvant or alum. Following booster immunizations, small samples of serum are collected and tested for reactivity to the disclosed polypeptides or their constituent epitopes. Examples of various assays useful for such determination include those described in: *Antibodies: A Laboratory Manual*, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press, 1988; as well as procedures such as countercurrent immuno-electrophoresis (CIEP), radioimmunoassay, radio-immunoprecipitation, enzyme-linked immuno-sorbent assays (ELISA), dot blot assays, and sandwich assays, see U.S. Pat. Nos. 4,376,110 and 4,486,530, each of which is incorporated by reference in their entirety.

Monoclonal antibodies (or fragments thereof), directed against epitopes of the disclosed polypeptides can also be readily prepared using well-known procedures, such as, for example, the procedures described in U.S. Pat. Nos. RE 32,011, 4,902,614, 4,543,439, and 4,411,993; *Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses,* Plenum Press, Kennett, McKearn, and Bechtol (eds.), 1980, each of which is incorporated by reference. Briefly, the host animals, such as mice, are injected intraperitoneally at least once, and preferably at least twice at about 3 week intervals with isolated and purified polypeptides optionally in the presence of adjuvant. Again, if peptide fragments are used they may need to be conjugated to a suitable carrier protein. Mouse sera are then assayed by conventional dot blot technique or antibody capture (ABC) to determine which animal is best to fuse. Approximately two to three weeks later, the mice are given an intravenous boost of pine tree polypeptides. Mice are later sacrificed and spleen cells fused with commercially available myeloma cells, such as Ag8.653 (ATCC), following established protocols. Briefly, the myeloma cells are washed several times in media and fused to mouse spleen cells at a ratio of about three spleen cells to one myeloma cell. The fusing agent can

be any suitable agent used in the art, for example, polyethylene glycol (PEG). Fusion is plated out into plates containing media that allows for the selective growth of the fused cells. The fused cells can then be allowed to grow for approximately eight days. Supernatants from resultant hybridomas are collected and added to a plate that is first coated with goat anti-mouse Ig. Following washes, a label, such as, ^{125}I-pine tree polypeptides is added to each well followed by incubation. Positive wells can be subsequently detected by autoradiography. Positive clones can be grown in bulk culture and supernatants are subsequently purified over a Protein A column (Pharmacia).

Monoclonal antibodies and specific-binding fragments of the invention can be produced using alternative techniques, such as those described by Alting-Mees et al., "Monoclonal Antibody Expression Libraries: A Rapid Alternative to Hybridomas", *Strategies in Molecular Biology* 3:1–9 (1990), which is incorporated herein by reference. Similarly, binding partners can be constructed using recombinant DNA techniques to incorporate the variable regions of a gene that encodes a specific binding antibody. Such a technique is described in Larrick et al., *Biotechnology,* 7:394 (1989).

It is understood of course that many techniques could be used to generate (antibodies against the polypeptides of the invention and that the above embodiments in no way limits the scope of the invention.

Nucleotides, Proteins, Antibodies, and Binding Proteins as Probes and Reagents

The disclosed nucleic acids, polypeptides, and antibodies directed against the disclosed polypeptides can be used in a variety of research protocols, such as in DNA arrays or as reagents. A sample of such research protocols are given in Sambrook et al. *Molecular Cloning: A Laboratory Manual,* 2 ed. Vol. 1–3, Cold Spring Harbor Laboratory Press, (1989), incorporated by reference. For example, the compiled sequences, polypeptides, etc., can serve as markers for cell specific or tissue specific expression of RNA or proteins. Similarly, this system can be used to investigate constitutive and transient expression of the genes encoding the cDNAs of SEQ ID NOS: 1–327 and the proteins encoded by these genes.

Further, the disclosed cDNA sequences can be used to determine the chromosomal location of the genomic DNA and to map genes in relation to this chromosomal location. The disclosed nucleotide sequence can be further used to identify additional genes related to the nucleotides of SEQ ID NOS: 1–334 and to establish evolutionary relatedness among species based on the comparison of sequences. The disclosed nucleotide and polypeptide sequences can be used to select for those genes or proteins that are homologous to the disclosed cDNAs or polypeptides, using well-established positive screening procedures such as Southern blotting and immunoblotting and negative screening procedures such as subtractive hybridization.

Method for Using Nucleic Acid Probes or Antibodies to Stage Embryos

Accurate staging of tree embryos is critical. It is known that different stages of tree embryos have different capacities as subjects for genetic transformation and genetic engineering. In addition, environmental requirements exhibited by embryos vary due to increasing physiologic age. Currently, the staging of tree embryogenesis is most accurately performed by an expert in the field who is very familiar with the morphological appearance of embryos at different stages. The cDNAs and related molecules of this invention can be used as markers for different stages of tree embryogenesis, thereby eliminating the need for a subjective eye to assess maturity and potentially allowing for more accurate staging of tree embryos. Moreover, by monitoring the expression of the underlying genes, it is possible to determine when an embryo has reached a certain level of development even if that level does not correspond to a visible difference in embryo morphology. The relational database of this invention aids the ability to monitor expression levels and tailor research approaches, such as the use of DNA arrays, to the specific needs of the objective, i.e., staging.

The information provided in this invention can be used in whole or in part to stage embryos. For example, one or a multiplicity of nucleic acid molecules from SEQ ID NOS: 1–327 having an expression profile consistent with a particular embryo stage can be used in this invention. A researcher may find it beneficial to use oligonucleotide probes or antibodies, for example, that specifically recognize proteins derived from genes expressed during middle embryonic stages, or that specifically monitor expression levels for embryos that have reached maturity associated with late developmental stages. A researcher can quickly determine that an embryo subset has progressed to or through an embryonic stage with the use of this invention and make appropriate changes in conditions if necessary, e.g. alter growth media or other environmental conditions.

Method for Monitoring Enhancing, or Determining Expression of Stage-Specific Genes

Expression patterns of SEQ ID NOS: 1–327 indicate that gene activation can be classified as stage-specific, such as in the case of SEQ ID NO: 327, otherwise known as "LP2-3." The promoter that drives such a gene can perform valuable functions. For example, a promoter from LP2-3 operatively linked to a reporter gene presented within an embryo system is expected to produce the reporter product under the conditions for expression of gene LP2-3. Thus, the system allows a rapid determination of stage specific embryos by a simple phenotypic reporter screen, perhaps by visualization of green fluorescent protein (GFP) or by loss of fluorescent protein product. Similarly, a set of promoters from known, differently staged genes operatively linked to reporter genes will be effective for monitoring developmental changes within the system as the embryos mature. The LP2-3 promoter is identified as SEQ ID NOS: 328–334 in Table I. The promoter expression pattern is that of the natively linked gene, LP2-3.

Virtually any indicator or reporter gene can be used for this approach or for other methods associated with this invention provided they are compatible with the system studied. Generally, reporter genes are genes typically not present in the recipient organism or tissue and which encode for proteins resulting in some phenotypic change or enzymatic property. Examples of such genes and assays are provided by Schenborn, E. and Groskreutz, D., Mol. Biotechnol., 13:29, 1999; Helfand, S. L. and Rogina, B., Results Probl. Cell Differ., 29:67, 2000; Kricka, L. J., Methods Enzymol., 305:333, 2000; Himes, S. R. and Shannon, M. F., Methods Mol. Biol., 130:165, 2000; and Leffel, S. M. et al., Biotechniques, 23:912, 1997, which are incorporated in their entirety by reference. In one embodiment of this invention, the reporter used is GFP, or any ariant of the fluorescent protein.

Additionally, one skilled in the art would recognize that a promoter, like that from LP2-3, has potential to stimulate production of products not ordinarily observed at a particular stage. A promoter derived from a gene that expresses during a known stage, for example an early stage, can be

operatively linked to a gene that does not normally express during that stage, yielding controlled expression of any targeted gene. It may be shown that earlier or later expression, or prolonged expression of a particular gene may give a desirable genotype or phenotype in a mature plant, may result in increased vigor in culture, or may be sufficient to alter the normal maturation process of the embryo. Prolonged expression of any desired gene also may be achieved from linking a constitutively expressed promoter to the targeted gene. Further, the ability to manipulate gene expression during embryogenesis allows for a detailed study of the effects of an individual gene or multiple genes on embryogenesis, leading to a better understanding of the developmental processes involved in embryogenesis.

Method of Correlating Gene Expression with Improved Tree Stock or Culture Conditions

Importantly, the cDNAs and related molecules of the invention can also be used as markers to examine genetic heterogeneity and heredity through the use of techniques such as genetic fingerprinting. These markers can also be correlated with improved agronomic traits including good initiation frequency, embryonic maturation, high frequency of germination, rapid growth rates, herbicide tolerance, insect resistance, pathogen resistance, climate and environmental adaptability wood quality, and wood fiber quality and content, to name a few. Additionally, the expression of these developmentally regulated genes can be compared among genetically identical clones grown under different culture conditions to determine the best protocols and media for somatic embryogenesis.

Cryogenic storage of pine embryos is effective for maintaining stocks of embryos determined by this invention to have the desired fitness traits or exist at the appropriate developmental stage. With such storage, one can specifically target desirable embryos for expansion many years after they are frozen. For example, a culture of somatic embryos can be divided into at least three portions, one of which is cryogenically stored, one which is used to study gene embryonic gene (and protein) expression, and one that is used to produce seedlings for field testing. Clones producing valuable mature plants could be selected and expanded from frozen stocks. Additional clones exhibiting similar expression patterns could be selected for future expansion and cultivation.

As will be evident to the ordinary practitioner, there are numerous ways in which the nucleic acids, polypeptides and antibodies of this invention might be used to characterize the gene expression of embryos. Ideally the stage-specific gene expression of embryos of several different genotypes and at several different stages of embryogenesis are characterized. For example, sets of oligonucleotide primers designed using any one of SEQ ID NOS: 1–327 may be used in RT-PCR assays to characterize expression of a gene product. In situ hybridization assays or antibody staining protocols may also be used to characterize RNA and/or protein expression and localization.

Embryos of the same genotype in which gene expression has been characterized may also used be to generate plantlets that are used in field testing. Once the embryos have developed into mature trees, the various genotype trees can be evaluated for important traits such as growth rates, herbicide tolerance, insect resistance, pathogen resistance, climate and environmental adaptability, wood quality, and wood fiber quality and content, among others. Finally the phenotypic data collected from the field testing can be correlated with gene expression during early embryogenesis to further enhance the database of the present invention. This will allow further identification of gene products which whose expression is correlated, either positively or negatively, with commercially valuable tree characteristics.

It will be clear to those skilled in the art that identification of such gene products can have several uses. Determining the correlation between a desirable phenotype and a genotype would allow for the "pre-selection" of tree embryos for field testing. It would also be useful in evaluating experimental tissue culture conditions for somatic embryogenesis; in other words, the expression level of a gene known to correlate with the development of trees with desirable characteristics could serve as the criterion on which culture media is evaluated, as opposed to assessing the phenotype of fully matured trees. The ability to evaluate culture conditions without having to develop fully mature trees and do field testing would save a great deal of research time and expense. And of course, the knowledge of the correlation between gene expression and desirable tree phenotypes would serve to identify target genes for genetic engineering.

Genetically Engineering Trees and Other Plants

There are several methods known in the art for the creation of transgenic plants. These include, but are not limited to: electroporation of plant protoplasts, liposome-mediated transformation, polyethylene-glycol-mediated transformation, microinjection of plant cells, and transformation using viruses. Because the invention is especially concerned with the transformation of woody species, the two prevalent methods for transforming forest trees, namely *Agrobacterium*-mediated transfer and direct gene transfer by particle bombardment, will be discussed in more detail, though it is understood that the present invention encompasses generation of transgenic plants via standard methods commonly known in the art.

Agrobacterium Mediated Transfer

A. tumefaciens and *A. rhizogenes* are two soil microorganisms that naturally infect a wide variety of plants including dicotyledonous plants, gymnosperms and some monocotyledonous plants. Infection by these organisms results in the growth of crown gall tumors or in hairy root disease, respectively. Each of these organisms carries a large plasmid, the tumor inducing (Ti) plasmid, in the case of *A. tumefaciens* and the root-inducing (Ri) plasmid in the case of *A. rhizogenes*. These plasmids have two critical features, a set of virulence genes and a segment of DNA called T-DNA that is delimited by conserved regions of approximately 25 base pairs known as the left and right borders. During infection, the T-DNA is transferred to the plant cell where it is able to stably integrate in single copy in the plant genome. Transfer of T-DNA requires the function of the virulence genes.

In its natural state, T-DNA contains genes that mediate progression of disease such as growth hormones or genes controlling root morphogenesis. Using recombinant DNA technology, however, T-DNA may be modified to contain an expression cassette encoding a foreign gene of interest. There are several T-DNA vector systems commonly in use for the transformation of plants. Several of these vector systems are reviewed in Hansen et al., *Current Topics in Microbiology and Immunology* 240: 21–57 (1999) which is hereby incorporated by reference. T-DNA vectors must include the left and right borders. In addition they must either be capable of replication in *Agrobacterium* or be designed so as to recombine with a plasmid that does so. The latter type of vector is known as a co-integrate vector. For transformation to proceed, there must also be a source of

virulence (vir) genes. The vir genes may be on the same plasmid with the T-DNA or more likely supplied by a helper plasmid. For example, binary T-DNA vector systems are comprised of two plasmids, one containing the vir genes and the other containing T-DNA. Some plants known to be recalcitrant to *Agrobacterium*-mediated transformation may be transformed if additional copies of some or all virulence genes are provided. Extra copies of VirG and VirE can be particularly useful.

Additionally, it is convenient to include in the T-DNA a selectable marker that will allow identification and selection of transformed plant cells. The selectable marker should be one that works in both *Agrobacterium* and the target plant. For example, the genes encoding chloramphenicol acetyltransferase and neomycin phosphotransferase are suitable marker genes that confer resistance to chloramphenicol and kanamycin, respectively. Additionally, a selectable marker may be provided on a separate T-DNA from the T-DNA encoding the gene of interest. Co-transformed T-DNAs can integrate at separate sites in the plant genome. This can be useful because it will later allow segregation of the marker gene in progeny enabling the generation of transgenic trees expressing the gene of interest but not the marker gene.

The gene of interest and the selectable marker genes must also be under the control of promoters that function in the transformed plant cell. Examples of suitable promoters include, but are not limited to: the abscisic acid (ABA)-inducible promoter from the early methionine (Em) gene from wheat (Marcotte et al., *Plant Cell* 1:976–979 (1989); the cauliflower mosaic virus (CaMV) 35S promoter (Odell et al., *Nature* 313:810–812 (1985); and the nopaline synthase (nos) promoter (Sanders et al., *Nucl. Acids Res.* 15(4):1543–58 (1987). Tissue-specific plant promoters or plant promoters responsive to chemical, hormone, heat or light treatments may be used. Additionally, the gene of interest may be expressed under the control of its endogenous promoter to ensure proper regulation.

The process of transformation requires plant cells that are competent and that are either embryogenic or organogenic. The plant cells to be transformed are then co-cultivated with *Agrobacterium* containing an engineered T-DNA vector system for 1–5 days. Following the co-cultivation period, the cells are incubated with the antibiotic against which the selectable marker confers resistance, and transformed lines are selected for further cultivation. The use of *Agrobacterium* mediated transfer in woody trees is described in Loopstra et al., *Plant Molecular Biology* 15:1–9 (1990), Gallardo et al., *Planta* 210:19–26 (1999) and Wenck et al., *Plant Molecular Biology* 39:407–419 (1999), each of which is hereby incorporated by reference.

Direct Gene Transfer by Particle Bombardment

Direct gene transfer by particle bombardment provides another method for transforming plant tissue. This method can be especially useful when plant species are recalcitrant to transformation by other means. In this technique a particle, or microprojectile, coated with DNA is shot through the physical barriers of the cell. Particle bombardment can be used to introduce DNA into any target tissue that is penetrable by DNA coated particles, but for stable transformation, it is imperative that regenerable cells be used. Typically, the particles are made of gold or tungsten. The particles are coated with DNA using either $CaCl^2$ or ethanol precipitation methods which are commonly known in the art.

DNA coated particles are shot out of a particle gun. A suitable particle gun can be purchased from Bio-Rad Laboratories (Hercules, Calif.). Particle penetration is controlled by varying parameters such as the intensity of the explosive burst, the size of the particles, or the distance particles must travel to reach the target tissue.

The DNA used for coating the particles should comprise an expression cassette suitable for driving the expression of the gene of interest. Minimally this will comprise a promoter operably linked to the gene of interest. As with *Agrobacterium* mediated transformation. Suitable promoters include, but are not limted to, the the abscisic acid (ABA)-inducible Em promoter from wheat (Marcotte et al., *Plant Cell* 1:976–979 (1989), the CaMV35S promoter (Odell et al., *Nature* 313:810–812 (1985), and the NOS:promoter (Sanders et., *Nucl. Acids Res.* 15(4):1543–58 (1987).

Methods for performing direct gene transfer by particle bombardment are disclosed in U.S. Pat. No. 5,990,387 to Tomes et al. Additionally, Ellis et al. describe the successful use of direct gene transfer to white spruce and larch trees in *Bio/Technology* 11, 84–89 (1993).

Researchers skilled in the area of DNA or gene transformation will recognize that additional procedures, or combination of procedures, may be useful for the successful tranformation of genetic stock.

Antisense Expression

The cDNAs of the invention may be expressed in such a way as to produce either sense or antisense RNA. Antisense RNA is RNA that has a sequence which is the reverse complement of the mRNA (sense RNA) encoded by a gene. A vector that will drive the expression of antisense RNA is one in which the cDNA is placed in "reverse orientation" with respect to the promoter such that the non-coding strand (rather than the coding strand) is transcribed. The expression of antisense RNA can be used to down-modulate the expression of the protein encoded by the mRNA to which the antisense RNA is complementary. This phenomenon is also known as "antisense suppression." It is believed that down-regulation of protein expression following antisense RNA is caused by the binding of the antisense RNA to the endogenous mRNA molecule to which it is complementary, thereby inhibiting or preventing translation of the endogenous mRNA.

The antisense RNA expressed need not be the full-length cDNA and need not be exactly homologous to the target mRNA. Generally, however, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous mRNA will be needed for effective antisense suppression. Preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. The length of the antisense sequence in the vector may be greater than 100 nucleotides. Vectors producing antisense RNA's could be used to make transgenic plants, as described above, in situations when desirable tree characteristics are produced when the expression of a particular gene is reduced or inhibited.

Methods

Tissue Samples

The cDNAs of the current invention can be derived from any sets of plant tissue. The cDNAs of SEQ ID NOS: 1–334, for example, were originally derived from embryonic tissues of pine tree embryos staged 1–9.9 as classified in Pullman and Webb TAPPI R&D Division 1994 Biological Sciences Symposium, pages 31–34, which is hereby incorporated by

reference. LPS and LPZ clones are derived from somatic and zygotic embryos, respectively. As noted, embryos may be of either somatic or zygotic derivation, and the embryos may be grown in either semi-solid or liquid tissue culture systems. Applicable methods for growing embryos in semi-solid or liquid tissue culture systems are disclosed in U.S. Pat. Nos. 5,036,007; 5,236,841; 5,294,549; 5,413,930; 5,491,090; 5,506,136; 5,563,061; 5,677,185; 5,731,203; 5,731,204; and U.S. Patent Application 60/212,651 filed Jun. 19, 2000, which are hereby incorporated by reference.

RNA Isolation

In one embodiment, RNA isolated from staged cell populations provides the starting material for reverse transcription, differential display, and cloning of amplified cDNA. Methods and kits for isolating total RNA from cellular populations, or for generating poly(A)+ RNA, are commonly known in the art. For example, several procedures for isolating RNA are disclosed in Chapter 4 of *Current Protocols in Molecular Biology* edited by F. A. Ausubel et al., John Wiley and Sons, Inc. (1987) (incorporated herein by reference). As an example, the TRI Reagent7 available from Molecular Research Center, Inc. (Cincinnati, Ohio) is a suitable reagent (used according to the manufacturer's instructions) for isolation of RNA from plant tissues.

Differential Display

Differential display provides a method to identify individual messenger RNAs that are differentially expressed among two or more cell populations. In the practice of the present invention, these cell populations may be provided by pine tree or other plant embryos of different developmental stages. The differential display procedure is taught in Liang et al., *Science,* 257:967–71 (1992) and in U.S. Pat. No. 5,262,311, which are hereby incorporated by reference. Briefly, mRNA sequences are PCR-amplified using two types of oligonucleotide primers known as "anchor" and "arbitrary" primers. Anchor primers are designed to recognize the polyadenylate tail of messenger RNAs. Arbitrary primers are short and arbitrary in sequence and anneal to complementary sequences in various mRNAs. Products amplified with these primers will vary in size and can be differentiated on an agarose or sequencing gel based on their size. If different cell populations are amplified with the same anchor and arbitrary primers, one can compare the amplification products to identify differentially expressed RNA sequences.

Cloning

PCR-amplified bands representing differentially expressed RNA samples are excised from the gel, transferred to tubes and reamplified using the same primer pairs and PCR conditions as used in the differential display procedure. Methods for the cloning of PCR products are commonly known in the art and there are several commercially available reagents and kits for cloning PCR products. For instance, the pCR-Scipt™ Cloning kit from Stratagene, La Jolla, Calif.) is suitable for this purpose. Using this kit, *E. coli* transformants containing plasmids with PCR fragment inserts can rapidly be identified using blue/white color selection followed by plasmid purification and restriction digests. The pCR-Script vector contains T3 and T7 polymerase recognition sites allowing for in vitro transcription of the inserted fragment.

Sequence Determination

Methods for sequencing DNA, including cloned PCR products, are commonly known in the art. The selection of cloning vectors having M13, T7 or T3 primer annealing sites flanking the PCR-amplified insert can be used in sequencing reactions directly. Most sequencing procedures in use today are modifications of Sanger's dideoxy chain termination sequencing reaction as disclosed in and Sanger et al., *Proceedings of the National Academy of Sciences,* 74:5463–5467 (1977), which is hereby incorporated by reference.

Homology Searching and Identification of Protein Coding Sequences

As understood by one of ordinary skill in the art, the sequence of a cloned cDNA insert obtained, may be compared against public databases such as Genbank to discern any identity or homology to known sequences. Programs, such BLAST, for performing such a search are available on the National Center for Biotechnology Information's web page. The results from Genbank search may reveal the potential function of a polypeptide or RNA molecule encoded by the cDNA. In addition to searching gene sequence database, the use of commercially available analysis software is well known in the art. For example, software packages such as the Wisconsin Package™ (Genetic Computer Group, Madison, Wis.) include programs such as FRAMES and CodonPreference that help to identify protein coding sequences in a query nucleotide sequence. FRAMES displays open reading frames for the six DNA translation frames, allowing one to quickly assess the presence or absence of stretches of open-reading frames that are likely to be protein encoding regions. CodonPreference is a more sophisticated program that identifies and displays possible protein coding regions based on similarity of the codon usage in the sequence to a codon frequency table (Gribskov et al., 1984).

EXAMPLE 1

Differential Gene Expression Analysis in Pine Tree Embryogenesis

cDNA libraries were prepared from staged pine tree embryos, as described above. The differential display technique was used to identify 327 novel cDNAs that were preferentially-expressed during early, middle, or late stages of pine tree embryogenesis, as set forth below. Clone nomenclature is divided into subsets based on tissue type; a clone is designated LPS to indicate somatic origins and LPZ for zygotic origins.

Plant Materials

Somatic embryos were collected at different stages of development. Cultures of somatic embryos of were initiated from Loblolly pine immature zygotic embryos as described by Becwar et al., *Forestry Science* 44:287–301 (1994) (incorporated by reference) or with minor modifications in media mineral composition. Somatic embryos were grown in cell suspension culture medium 16 (Pullman and Webb, Tappi R&D Division 1994 Biological Sciences Symposium) and a maturation medium similar to that of a standard maturation media. Resulting somatic embryos were selected and classified as stages 1–9 according to morphological development following the teachings of Pullman and Webb, Tappi R&D Division 1994 Biological Sciences Symposium pp. 31–34. Somatic embryos were sorted into tubes containing the same stages and stored at −70° C.

RNA Isolation

Total RNA was isolated from all stages of somatic embryos of loblolly pine and grouped into early, middle, and

late phases of development. The early phase is represented by a liquid suspension culture containing embryos of stages 1 through stage 3. Middle phase contains embryos of stages 4 through stage 6, while stages 7 through 9 formed the late phase. 60–100 mg aliquots of staged frozen embryos were ground in 1.0 ml of TRI Reagent® Isolation Reagent (Molecular Research Center, Inc.), a commercial product that includes phenol and guideline thiocyanate in a monophase solution and extracted according to the manufacturer's instructions.

Reverse Transcription of mRNA (RT-PCR)

The total RNA was used as a template to synthesize single stranded DNA mediated by MMLV reverse transcriptase (100 U/μl). The method involves the reverse transcription by PCR of the mRNA with an oligo-dT primer (H-T_{11}G: 5' B AAGCTTTTTTTTTTTG 3') anchored to the beginning of the poly(A) tail, followed by a PCR reaction in the presence of a second short (13-mer) primer which is arbitrary in sequence [AP_1 (5' B MGCTTGATTGCC-3') or AP_2 (5' B MGCTTCGACTGT-3')]. Reverse transcription and Differential Display were conducted using the GenHunter RNAimage Kit I.

A 19 μl reverse transcription reaction (10 μl sterile water, 2.0 μl 5× RT buffer, 1.6 μl dNTP (250 μM), 2.0 μl anchored primer (2.0 μM), 2.0 μl RNA template at 100 ng/μl) was prepared for each embryo phase sample. The reaction mixture was heated to 65° C. for 5 minutes in a thermocycler, cooled to 37° C. and paused after 10 minutes while 1.0 μl MMLV was added. The program was allowed to resume at 37° C. for 50 minutes. The reaction was then heated to 75° C. for 5 minutes, cooled to 4° C. and stored at −20° C.

Incorporation of Radiolabeled Nucleotides by PCR

Differential Display PCR was performed in a 20 μl reaction containing 2 μl of the reverse-transcribed cDNA template; 10 μl sterile water 2.0 μl 10× PCR buffer, 1.6 μl dNTP (25 μM), 2.0 μl anchored primer H-T11 G, (2.0 μM), 2.0 μl 13 mer arbitrary primer (AP_1 or AP_2 (2.0 μM), 0.2 μl Taq DNA polymerase, and 0.2 μl α^{32}P-dATP (2000 Ci/mmole). The cDNA was amplified by PCR: 94° C. for 3 minutes, 40 cycles of 94° C. for 30 seconds, 40° C. for 2 minutes, and 72° C. for 30 seconds, followed by 72° C. for 5 minutes. The reaction was cooled to 4° C. and stored at −20° C.

Differential Display

The PCR products were separated on a Stratagene (La Jolla, Calif.) pre-cast 6% polyacrylamide sequencing gel at 30 watts constant power for approximately 2.5 to 3 hours. 3.5 μl of sample was mixed with 2.0 μl of loading dye and incubated at 80° C. for 2 minutes immediately before loading onto the gel. The gel was rinsed in water and dried. Dilute ^{33}P-dATP with loading dye was spotted at the corners as alignment markers and the gels were exposed to Kodak BioMax™ autoradiography film. An exemplary gel is shown in FIG. **1**.

Bands that appeared to be possible markers for phase specific gene expression were marked on the film and aligned over the gel. The bands were excised by cutting through the film. The gel pieces were scraped from the gel and transferred to tubes and re-amplified using the same primer pairs and PCR conditions as used for incorporation of radiolabeled nucleotides.

Cloning of DNA Fragments from Differential Display

The PCR products from the gel fragments were purified, polished, ligated and cloned into XL 10-Gold Kan ultracompetent cells by heat shock with the Stratagene pCR-Script Amp SK(+) Supercompetent Cell Cloning Kit according to manufacturer's instructions. The transformed cells were spread on LB agar plates containing ampicillin, IPTG, and X-Gal each at 50 μg/ml. The plates were incubated overnight at 37° C. Plasmids containing PCR inserts were identified using blue-white colony screening. The presence of inserts was confirmed by digesting the clones with restriction endonucleases, Msc I and Nla III, followed by standard DNA gel electrophoresis. Transformants representing early, middle, and late phase embryos were sequenced using standard dideoxy protocols known in the art with the T3 primer.

Sequence Analysis

All sequences were analyzed using a program-database pair search of the NCBI BLAST 2.0 server, blastn-nr, blastn-others ests, and blastx-nr. In each case, the query sequence was filtered for low complexity regions by default and entered in FASTA format. Other formatting options were set by default; alignment view-pairwise, descriptions-100, and alignments-50. Using these parameter settings, significant similarity to known DNA, RNA, or protein sequences was found for several of the nucleic acid molecules of SEQ ID NOS: 1–334, for example, those described herein. (Alignment data not shown).

EXAMPLE 2

Characterization of Full Length LP2-3 cDNA Sequence

SEQ ID NO: 327, designated LP2-3, was first identified through differential display with T_{12}MG and AP_1 primers (GeneHunter). The differential display band appeared to be present only in liquid suspension cultures of Loblolly Pine somatic embryos. The conditions for mRNA isolation, reverse-transcription, differential display-PCR, and gel separation/visualization for producing this band were all as described in Example 1. Likewise, the band containing the original LP2-3 fragment was excised from the differential display gel, amplified, and cloned into pCR-Script AMP SK(+) according to standard protocols known in the art.

Northern Hybridizations Demonstrating Early-Specific Expression

Northern analysis demonstrated that the LP2-3 differential display clone hybridized to an approximately 1.2 Kb mRNA from liquid suspension culture embryos but was undetectable in late (6–9) stage embryo RNA. (FIG. **11**) In general, LP2-3 is most highly expressed in early stage embryos in liquid culture. LP2-3 mRNA is found most abundantly in early stage somatic embryos, especially for embryos grown in liquid multiplication medium. (FIG. **12**) Further, transcription decreases rapidly as embryos are transferred to maturation medium (stage 3 and stage 4) and begin to mature. LP2-3 transcripts are virtually undetectable at stage 6–9 somatic embryos grown on maturation medium. (See FIG. **12**) Additional studies indicate that LP2-3 mRNA is expressed zygotically, particularly in early stage zygotic embryos, but is undetectable in mature vegetative tissues. (FIGS. **13** and **14**) Specifically, the signal intensity from liquid suspension somatic embryo RNA was about 3 times greater than the signal from the analogous stage 1 zygotic embryo RNA. (FIGS. **13** and **14**) LP2-3 transcripts were not detectable in total RNA from needles, stems, or roots of one year old seedlings, including those exposed to cold, ozone, wound stresses, or the hormone jasmonic acid (not shown).

LP2-3 Differential Display and 'Full-Length' cDNA Sequences

A 'full-length' cDNA was captured from SMART™ cDNA made from somatic embryo liquid suspension by using a biotinylated LP2-3 differential display fragment as a capture probe. The "full-length" cDNA was cloned and sequenced according to standard protocols known in the art. This sequence was designated at LP2-3^{+}.

GenBank blastx searches conducted with the above sequence translated in all 6 reading frames indicated that LP2-3^{+} likely encodes a member of the major intrinsic protein family. This family of proteins encodes membrane channels for the transport of water and/or ions across cell membranes. They may play a significant role in osmoregulation and may play a role in the cellular responses to water and salt stresses. As is known in the art, the MIPs are induced by dessication, flooding, and high levels of the plant hormone ABA. In contrast, the LP2-3 sequence was not detected in desiccated late-stage embryos which have high levels of ABA and, thus, appears to be regulated by some embryo-specific signal.

EXAMPLE 3

Hypothesis Development for Improved Protocols

Currently the improvement of tissue culture practices arises via hypothesis, evaluation and adoption. Hypotheses arise from observation of size, shape, weight, etc. and physiological measurement of ion or sugar content (FIG. **6**, box 1). These observations are limited in scope and this limits the improvements that can be made to the tissue culture process. Gene expression is closely linked to metabolic condition, thus the observation of which genes are induced or repressed under a given growth condition, naturally, on the tree, or in a culture vessel, provides insight into the metabolic state of the embryo. This information can be used to create new hypotheses that can be evaluated by modifying tissue culture.

To this end, mRNA levels of two cDNAs (LPZ-202 and LPZ-216), similar to "Late Embryogenesis Abundant" (LEA) proteins, identified in other plants, were monitored. These genes are induced by the plant hormone ABA. Two peaks of mRNA were observed in these clones rather than the typical single peak in most plants. (See FIG. **4** for clone LPZ-216; clone LPZ-202 is similar but data is not shown.) It was subsequently confirmed that two peaks in ABA activity are observed during development and that these correspond in timing to the elevation in mRNA for LPZ-202 and LPZ-216. Thus mRNA abundance profiles are providing insight into embryo physiology. (See FIG. **7**) The effect of giving two pulses of ABA to our somatic embryos is assessed; a tissue culture modification that we might not have considered as important had the gene expression data been unavailable. Internal data shows fluctuations in the abundance of mRNA for cDNAs listed in this collection (data not shown.)

Zygotic and Somatic Loblolly Pine Embryos

Loblolly pine cones were collected weekly from a breeding orchard near Lake Charles, La., and shipped on ice for experimentation. Embryos were excised and evaluated for developmental stage (Pullman et al. 1994). Stage 9 embryos were separated by the week they were collected—9.1 (week 1), 9.2 (week 2), etc. Staged zygotic embryos were sorted into vials partially immersed in liquid nitrogen and stored at −70° C. Somatic embryos for loblolly pine were initiated as described by Becwar et al. (1995) or with minor modifications. Somatic embryos were grown, selected, and staged as described by Pullman et al. (1994) and stored at −70° C.

cDNA Probe Preparation and Hybridization

30 ng of purified Lea protein cDNA fragments was labeled with ^{32}P dCTP using the Ready-To-Go cDNA Random Labeling kit (Pharmacia). The labeled cDNAs were purified using NICK Column (Pharmacia) and heat denatured for hybridization. The RNA slot blot was pre-hybridized in hybridization buffer (0.5 M sodium-phosphate, pH 7.2, 5% SDS, and 10 mM EDTA) at 65° C. for 2 hours in a hybridization oven (Model 400, Robbins Scientific, Sunnyvale, Calif.) and the hybridized in the same conditions with the cDNA probes. After hybridization, the membranes were washed at 65° C. in 0.2×SSC and 0.1% SDS. Each wash was 15 min. The membranes were then exposed to Image Plate.

The probes can be stripped from the RNA slot blot by pouring boiling 0.5% SDS onto the membrane twice and incubating without heating for 30 min. The stripped blot was then exposed to Image Plate for overnight to check the completeness of the de-probing before next round of hybridization.

To ensure the equal loading of the each RNA sample, the same membranes were stripped and hybridized with a ^{32}P-dCTP labeled 26S ribosomal rDNA fragment. These results were used as controls to normalize the Lea protein gene expression levels.

As a means of evaluating the usefulness of these arrays, we followed the expression of three cDNAs that have strong sequence similarity to late embryo-abundant proteins, (Lea) proteins from cotton (Baker et al 1988). Lea proteins and mRNAs appear in embryos at a stage when ABA is high and the genes can be induced in vegetative tissue by application of ABA. The transcript level of Lea genes LPZ-202 and LPZ-216 showed two peaks, rising from stage 5 and returning to a base line about stage 9.2 then rising again around stage 9.5. (See FIG. **4** for clone LPZ-216).

To confirm the fluctuation in lea transcript levels by Northern analysis. RNA was extracted from zygotic embryos at different stages of development. A pine 'dehydrin' cDNA from the North Carolina State University cDNA collection was used as probe for some experiments. Dehydrins are a class of lea protein, originally identified as water deficit inducible proteins. Since the expression of this class of protein is well characterized, in contrast to our lea genes, the dehydrin expression profile could act as a reference point. After probing with dehydrin, blots were stripped and probed with a 26S rDNA probe from *Arabidopsis* to check the loading of the original gel. The normalized expression pattern of dehydrin in the zygotic embryogenesis is illustrated in the top panel of FIG. **4**. The expression of the dehydrin gene was induced at stage 5 and reached a peak at stage 6. It declined at stage 7–8, just prior to the onset of the desiccation. Then the mRNAs level remained low from stage 9.1 through 9.5. The dehydrin mRNA levels rose again late in development, from stage 9.6 on, apparently dropping in very late development. A similar pattern of expression was observed in a parallel experiment when our lea-like clone, LPZ-216, was used as a probe.

This pattern reveals two significant peaks at the early development of the embryos and high expression levels for the stage 9.6 and beyond. The expression pattern of these two lea genes in loblolly pine embryos is consistent with the changes in ABA concentration observed in pine during embryogenesis. (See FIG. **5**)

EXAMPLE 4

Evaluation of Metabolic State of Somatic

Embryos as Compared to Zygotic Embryos for Fitness Determination

The model and goal for somatic embryogenesis is to produce an embryo that in vigor, germinatability, etc., resembles a zygotic embryo. Standard measurements reveal relatively little about the embryos; thus the metabolic state of somatic and zygotic embryos is unknown. The metabolic state of zygotic (natural) embryos can be evaluated by DNA arrays containing the cDNA clones described in this application. A database of mRNA levels for the genes represented on the DNA arrays can then be established. Embryos growing under a new tissue culture protocol (FIG. **6**, box #2) can be evaluated by DNA array southerns (FIG. **6**, box #3). The array elucidates patterns of gene activity and reveals whether those patterns are similar to the natural state (FIG. **6**, box #4). The germination, or further development can be checked (FIG. **6**, box #5) to confirm the conclusion. Where a link between specific gene activity and embryo performance has been demonstrated, protocols can be modified with efficiency as seen in FIG. **6**, box 6.

To illustrate this process, elevation of plant hormone ABA in maturation medium was evaluated as a protocol modification, as described below. This modification proved beneficial, elevating the number and quality of the embryos produced. The mRNA abundance for cDNAs was assessed by DNA array using RNA isolated from control and elevated ABA conditions; several differences were observed in the mRNA levels of specific genes. Further, abundance of mRNA in the elevated ABA condition, more closely resembled the mRNA abundance observed for the these same genes in zygotic embryos. Thus a protocol which produces higher quality embryos produces, in these embryos, a mRNA profile that more closely resembles that observed in natural embryos.

Zygotic and Somatic Loblolly Pine Embryos

Loblolly pine cones were collected weekly from a breeding orchard near Lake Charles, La., and shipped on ice for experimentation. Embryos were excised and evaluated for developmental stage (Pullman et al. 1994). Stage 9 embryos were separated by the week they were collected—9.1 (week 1), 9.2 (week 2), etc. Staged zygotic embryos were sorted into vials partially immersed in liquid nitrogen and stored at −70° C. Somatic embryos for loblolly pine were initiated as described by Becwar et al. (1995) or with minor modifications. Somatic embryos were grown, selected, and staged as described by Pullman et al. (1994) and stored at −70° C.

Mass Isolation of Genes Differentially Expressed in Loblolly Pine Zygotic Embryos

The following RNA differential display method is sensitive enough to produce banding patterns from one mid- to late-stage embryo or 10–20 early stage embryos. This technique, which extracts mRNA directly from tissue using oligo(dT) beads, avoids losses inherent in conventional RNA extraction methods, is fast, reliable, and inexpensive. Differences in gene expression during development, as well as between somatic and zygotic embryos, can be easily detected.

To achieve these results, 50–100 μl lysis buffer containing 100 mM Tris-HCl, pH 8.0, 500 mM LiCl, 10 mM EDTA, 1% SDS and 5 mM DTT was added to 10–100 mg of staged embryos in a 1.5 ml tube. The mixture was ground thoroughly with an electric drill containing a plastic pestle bit (VWR, Cat# KT95050-99) that had been sterilized by autoclaving. An additional 50–100 μl lysis buffer was added and ground briefly. The grinder and vortex was washed with 100 μl lysis buffer. If multiple samples were processed, each is stored on ice until ready for the next step. The grinding tip was washed with sterile water and dried for the next sample.

After all the samples were ground, they were spun at 4° C. for 15 minutes in a bench top centrifuge at 14,000 rpm. 8 μl oligo(dT) coated Dynal beads (mRNA DIRECT Kit, Dynal, N.Y.) was placed in a 1.5 ml tube. The Dynal beads were washed twice with a 100 μl of the above mentioned lysis buffer and suspended in an equal volume of the lysis buffer used in tissue grinding. If more than one sample is handled, the beads for all the samples can be washed together and dispensed in several 1.5-ml tubes. The cleared embryo lysate (after centrifugation) was added to the beads and mixed well.

The mixture was then incubated on ice for 5 min., placed on a magnetic stand (Promega) for 5 min., and partially dried by careful removal of the liquid. To this, 100 μl of washing buffer with LiDS containing 100 mM Tris-HCl, pH 8.0, 0.15 mM LiCl, 1.0 mM EDTA, and 0.1% SDS was added. (mRNA DIRECT kit.) The mix was transferred to a 200 μl PCR tube. The beads were washed once with 100 μl washing buffer with LiDS and once with 50 μl washing buffer containing 100 mM Tris-HCl, pH 8.0, 0.15 mM LiCl, and 1.0 mM EDTA. (mRNA DIRECT kit.) The beads were then washed quickly with 20 μl 1× RT Buffer (25 mM Tris-HCl, pH 8.3, 37.6 mM KCl, 2.5 mM MgCl2, and 5 mM DTT) and 20 μl RT Mix containing 1× RT Buffer and 20 μM dNTP was added. The tube was heated at 65° C. for 5 min. and cooled to 37° C. 1 μl MMLV reverse transcriptase (Promega) was added and the mixture was incubated at 37° C. for 1 h. with occasional shaking. Next, 20 μl of water was added to the RT reaction, mixed and a 1.0 μl to 20 μl aliquot of the PCR mix containing 1× Perkin-Elmer PCR buffer, 2.0 μM dNTP, 1.0 μM T12VN, 0.2 μM arbitrary 10-mer, 1 unit AmpliTaq (Perkin-Elmer), 50 μCi α^{35}S-dATP (Amersham) was taken. PCR using temperature settings of 94° C. 30", 40° C. 1', 72° C. 2', 40 cycles, and 72° C. 10' extension was performed with the Perkin Elmer 9600 Thermal Cycler. All PCR product was run on appropriate gels for band visualization.

cDNA cloning of Differential Display Bands

All dried gels were marked with radioactive ink prior to film exposure for proper alignment between the X-ray film and the dried gel plate. Appropriate bands were marked by puncturing. A scalpel blade was used to score the gel around each band to be excised. The excised gel pieces were placed into a PCR tube containing 2 μl water. PCR was performed using a 50 μl PCR mix (same as for differential display with the following modifications: the primer concentration was 1 μM, and the dNTP concentration was 200 μM; no α^{35}S-dATP is added.) The cycle settings were the same as above.

A portion of the PCR products was run on a gel to determine amount and size of PCR products; DNA that did not correspond to the size of the original differential display band was discarded. The remaining PCR fractions were purified using CHROMA SPIN-100 columns (Clontech, Palo Alto, Calif.) according to the manufacturer's instructions. The purified PCR fragments were cloned into the pCR2.1 TA cloning vector (Invitrogen) according to Invitrogen cloning protocols supplied with the vector. The only variation from the standard protocol was an increase in the molar concentration of PCR product to vector (over 100-fold); multiple insertions were not found to be a problem. All

ligations were performed at 16° C. overnight, transformed into *E. coli* strain DH5α, and plated onto LB with X-gal/IPTG.

Five colonies were chosen for PCR verification; PCR products of expected size were selected. About 10 μl of the 30 μl PCR reaction was simultaneously digested with Nla III and Mse I overnight at 37° C. (a 5 h digestion was used as well.) cDNA clones were selected according to the colony PCR and the restriction enzyme digestion pattern.

The differential display protocol for finely staged zygotic embryos of loblolly pine as described above, has produced more than 600 differential display patterns and more than 60,000 bands. Within that set of bands, we have identified bands that increased and/or decreased during embryo development. From those bands, cDNA clones of this invention were isolated and sequenced.

Detection of Gene Expression by Micro-Array Assay

In order to verify expression patterns of the cloned DNA in loblolly pine embryos a micro-array assay was developed. The cloned cDNAs were amplified by PCR and adjusted to equal concentrations (0.1 μg/μl). The cDNAs were then dispensed in the wells of a 384-well plate, denatured in 0.3 M NaOH at 65° C. for 30 min. and neutralized with 2 volumes of 20× SSPE mixed with 0.00125% bromophenol blue and 0.0125% xylene cyanol FF (5% gel loading dye). The denatured DNAs were then blotted on to Hybond N+ membranes (Amersham) as arrays using a VP 386 pin blotter (V&P Scientific, Inc., San Diego, Calif.). Each DNA was dot-blotted four times as a quartet on the membrane. An example of quartet spotting is seen in FIG. **7**. Each dot is about 1.2 mm in diameter and contains about 3 ng of DNA. DNA was then cross-linked to the membrane at 120,000 mJ/cm2 in a CL-1000 UV-linker. (Strategene, Inc., Upland, Calif.) The dot image of each membrane was scanned, numbered and saved in computer for later use in data digitizing.

The cDNA array membranes were pre-hybridized in hybridization buffer (0.5 M Na-phosphate, pH 7.2, 5% SDS, and 10 mM EDTA) at 65° C. for 30' in a hybridization oven (Model 400, Robbins Scientific, Sunnyvale, Calif.) and then hybridized under the same conditions with total cDNA probes made from mRNA. The membranes were washed twice at room temperature in 2× SSPE and 0.1% SDS, twice in 0.5× SSPE and 0.1% SDS, and twice in 0.1× hybridization buffer. Each wash was roughly 20 min. Each membrane was then exposed to Kodak Biomax MR films.

The total cDNA probes referred to above were made by initially creating the first strand cDNA. This was accomplished by mixing loblolly pine embryos (0.05–0.1 gm fresh weight) with 100 μl lysis buffer (containing 100 mM Tris-HCl, pH 8.0, 500 mM LiCl, 10 mM EDTA, 1% SDS and 5 mM DTT) in a 1.5 ml Eppendorf tube. The mix was then ground with an electric drill as described above. Another 100 μl lysis buffer was added and the lysate was ground again briefly. The drill pestle was washed with 100 μl lysis buffer that was pooled with the lysate. After centrifugation at 14K at 4° C. for 15 min. in a Beckman bench top centrifuge, the clear embryo lysate was mixed with 10 μl Dynal beads washed twice with lysis buffer. The suspension was incubated on ice for 5 min., with occasional mixing to allow binding of Poly (A) RNA to the oligo (dT) on the beads, and then left on a magnetic stand at room temperature for another 5 min. The liquid was removed and the beads were moved to a 0.2 ml PCR tube by suspending in 100 μl lysis buffer.

The beads were washed twice with 100 μl of washing buffer with LiDS and once with 50 μl of washing buffer. The mRNA was eluted from the beads in 6 μl water at 65° C. for 2'. One μl T21VN primer (10 μM) and 1 μl SCSP oligo (cap switch primer, 5'-ctcttaattaagtacgcgggg-3', 10 μM) were added to the mRNA eluate. The mixture was incubated at 70° C. for 2' and cooled on ice. Three μl 5× First Strand Buffer, 1.5 μl DTT (20 mM), 1.5 μl dNTP (10 mM each) and 1 μl MMLV Superscript II (Gibco BRL) were added to the mRNA-primer mixture followed by incubation at 42° C. for 1 h to synthesis first strand cDNAs. The cDNA was heated to 72° C. for 1 min. to degrade RNA and then diluted to 100 μl with water. The lysis buffer, washing buffer and Dynal beads are components of the mRNA DIRECT kit (Dynal, N.Y.). The first strand buffer (5×), 20 mM DTT and 10 mM dNTP are components of the SMART PCR cDNA synthesis kit (Clontech, Palo Alto, Calif.).

The first strand cDNAs synthesized as described above contains a T21VN sequence at their 5' ends and the SCSP sequence (see "SMART™ cDNA, Clontech, Palo Alto, Calif.) at their 3' terminals. Total cDNA probes were made by PCR amplifying the first strand cDNAs using SMART cDNA PCR (Clontech, Palo Alto, Calif.) in the presence of labeling agent. Five 5 μl first strand cDNA solution was mixed with 5 μl 10× KlenTaq PCR buffer (Clonetech), 5 μl dATP+dGTP+dTTP (5 μM each), 1 μl T21VN primer, 1 μl SCSP oligo, 1 μl KlenTaq Mix, 5 μl 32P-dCTP (10 mCi/ml, Amersham) and 27 μl water. The PCR was performed using the setting of 94° C. 2', 15 cycles of 95° C. 15", 52° C. 30", 68° C. 6'. The PCR products were purified using NICK column (Pharmacia) according to the manufacture's instructions.

Currently, high-density array Southerns for both somatic and zygotic embryos at all the developmental stages have been performed. The dot array Southern data indicate that gene expression of late stage somatic embryos resembles middle stage zygotic embryos; many transcripts present during late zygotic embryogenesis (ZE) are absent in somatic embryos and late stage somatic embryo gene expression patterns resemble the patterns of middle stage zygotic embryos.

Cairney et al. (*In Vitro Cell. & Devel. Biol.—Plant.* 36:155–162 (2000); *Appl. Biochem. Biotech.* 77–79:5–17 (1999)) have discussed how this gene expression information may be used to improve the process of somatic embryogenesis; the references are incorporated in their entirety. As shown in FIG. **2**, the high-density array Southerns allows rapid evaluation of embryos subjected to protocol changes. Following the expression of a known gene permits inferences about metabolism and is very valuable in developing media-improvement hypotheses. Further, detailed gene expression studies may help by providing an understanding of the timing and location of gene expression (e.g., in situ hybridization). The isolation of key genes also provides the ability to monitor the expression of these genes as stage specific markers and allows protocol variations to be quickly evaluated.

EXAMPLE 5

Identification of Markers for Superior Performance in Tissue Culture

The evaluation of tissue culture modifications for pine somatic embryogenesis, depicted in FIG. **8**, is typically a lengthy process. However, where molecular tools are available, potentially improved media or genotypes can be discerned more rapidly, thereby avoiding the months of costly evaluation. (See FIG. **8**) Table 5 illustrates this proposition.

Table 4 describes several publicly available clones, Lec, Fie, and Pkl, used to provide a representative model for this example. Any clone within Table 1, SEQ ID NOS: 1–327, can be substituted for those in Table 4 to assay increased performance in tissue culture. Any promoter within Table 1,

SEQ ID NOS: 328–334, can be incorporated with those in Table 4 or SEQ ID NOS: 1–327 to assay increased performance in tissue culture. In this scenario, Table 5, a representation of the information contained in FIG. **9**, shows performance of selected genotypes (260, 480, 499, and 500) in various media (1133 or 16) determined by the total number of embryos produced per medium as described by Pullman and Webb (1994), incorporated herein. Embryo maturation was determined by the presence of recognized morphology according to methods previously mentioned above. (Pullman and Webb, (1994)) Genotypes that produced high, medium, and low numbers of embryos were selected for RNA extraction. Gene expression assays, such as DNA arrays, Northern blots, slot blots, etc., were used in attempt to correlate embryo performance with mRNA abundance for selected genes. In the example shown in FIG. **9** and Table 5, expression of loblolly pine genes, designated as Lec, Fie, and Pkl, obtained from the Pine Gene Discovery Project, was evaluated. The preliminary correlation appears to be that the high levels of the Lec gene's mRNA correlates with greater number of pine embryos. (See table 5.) These experiments can be further expanded to incorporate additional or alternative genotypes with the prospect of identifying a large collection of gene indicators of good or poor performance in tissue culture based on high or low mRNA levels. It is clear from the above that this approach, using the sequences disclosed in this application, can evaluate a genotype entering tissue culture, saving both time and expense.

Somatic Embryos

Immature zygotic seeds were collected from loblolly pine genotype 260 (mother tree BC-3, Boise Cascade). Somatic embryos were initiated as described by Becwar et al. (1990) or with modifications in media mineral composition. The early stage somatic embryos were grown in cell suspension culture medium 16 and sub-cultured every week (Pullman and Webb, 1994). The embryos collected from the suspension, which include stage 1 and stage 2 somatic embryos, are referred to as stage S embryos. At the end of the subculture week, the somatic embryos in the suspension were settled in a cylinder and transferred to maturation medium 240 (Pullman and Webb, 1994). Resulting somatic embryos were selected, staged, sorted into vials containing the same stage, and stored at −70° C. until analyses were performed.

Probes

For the following example analysis RNA was isolated from embryos at different stages in development, early stage somatic embryos and late-stage somatic embryos. The cDNA probes used in this example are not contained in the SEQ ID NOS: 1–327, but rather, are generic, publicly available pine sequences obtained from the Pine Gene Discovery project. These clones are homologs to the well-studied *Arabidopsis* genes that have been shown to have significant influence on embryo development in this plant. The pine clone names (first column) and corresponding references for the *Arabidopsis* homologs are shown in Table 4. The three clones listed, Lec, Lie, and Pkl, are for representative purposes within this example and it will be clear to one skilled in the art that any of the SEQ ID NOS: 1–327 could be substituted for those here as all will help identify conditions for improved performance in culture.

Probes were made by preparation of DNA using Wizard Minipreps (Promega, Madison, Wis.) and cDNA inserts isolated by restriction enzyme digestion. For the cDNA probes, 50 ng of the isolated cDNA insert DNA was used to make ^{32}P-labeled probes with Ready-To-Go DNA labeling beads (Amersham Pharmacia Biotech) according to manufacturer's instructions. Blots were prehybridized (7% SDS, 1% BSA, 0.25 M $NaPO_4$ (pH 7.2), 1.0 mM EDTA) for 3 hours at 65° C. and hybridized in fresh buffer at 65° C. for 12 to 18 hours (4). Each blot was washed 6 times with the following conditions: 1) RT, 2×SSC, 0.1% SDS, 15 min; 2) RT, 2×SSC, 0.1% SDS, 30 min; 3) 42° C., 0.2×SSC, 0.1% SDS, 15 min; 4) 42° C., 0.2×SSC, 0.1% SDS, 30 min; 5) 60° C., 0.2×SSC, 0.1% SDS, 30 min; 6) 60° C., 0.2×SSC, 0.1% SDS, 30 min. Blots were exposed to a phosphorimaging plate for 10 minutes. Screens were read with a BAS1800 (software v1.0) and images were manipulated with ImageGauge (v2.54) (Fuji Photo Film Co., Ltd., Kanagawa, Japan).

The hypothesis tested within this example is that genotypes that produce large numbers of embryos have high Lec expression and low Pkl expression, poor genotypes have the opposite pattern, and that Lec and Pkl expression act as indicators of embryogenic potential. FIG. **9** shows that Lec is not expressed in late stages of embryogenesis in somatic embryos. The Lec gene is expressed throughout embryogenesis in *Arabidopsis*. The blot reveals that the Lec gene is a useful early expression marker for embryogenesis. One interpretation of these results is that the somatic embryos do not express Lec in the manner that Lec is expressed in zygotic embryos, i.e. the use of Lec expression has highlighted a defect in gene expression in somatic embryos. This defect could be used to identify desirable genotypes, i.e. those likely to progress through development and produce a large number of healthy plantlets compared to undesirable genotypes that will cease development prematurely or produce low numbers of plantlets. This is an example of the principle described pictorially in FIG. **8**.

The results described in the previous section of Example 5 reveal ways in which gene expression analyses can be used to improve somatic embryogenesis based on several genes. However, this principle applies as well when the assay is expanded to determine the expression of hundreds or thousands of genes simultaneously (e.g. by DNA arrays). We can create hypotheses which state that expression of a single specific gene can be used to determine the potential of a culture, or hypotheses that state that the expression of a group of genes (e.g., hypothetical genes A, B, C, D, E, F) acts as an indicator of high embryogenic potential. For example, all these genes may be expressed at a high level in cell lines that produce large numbers of embryos, thus we would select cell lines which exhibited this characteristic. Alternatively specific levels of expression for genes A, B, C, D, E and F may be required and a combination of high and low expression of particular genes will identify desirable cultures. Alternatively, experience will determine that certain exceptions can be tolerated.

While the previous paragraphs discuss numbers of embryos produced, the principle applies to ANY desired characteristic: by establishing a correlation of gene expression with e.g., germination potential, embryo size, growth of plantlets in their first year, disease resistance of mature plants, environmental hardiness or wood quality. Any trait where could be evaluated by these gene expression assays and correlations with gene expression established, resulting in a molecular tool which could be used to predict desirable characteristics. Explicitly, we could use these gene expression tools to select cell lines which will produce high quality plantlets months before they grow into plantlets, or cell lines or juvenile plantlets which will produce hardy trees with desirable wood quality, years before these traits are expressed.

TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:1	Late	LPS-001	GGTACTCCACCGTAATAACCCTTGGGAAATAGCCTATGATCCAGGGGAGGCAACC
			ACCTATATCATTGACAACAGCGAAAAATGTGGCGCAAGAAGTTTCACATACAATTCA
			TGGTTACAAAGATCACATACCAGGTGTTGGAGCAGATTCGATAGATATTGAAGATAT
			GAAGCCAAGGAGTGGAGCAGTTATTGAAAAGGGCACAAAAAAATTTGCCATTTACA
			AAGATGAAAATGGGCTGATTCACAAATACTCGGCAATATGCCCACACATGAACTGT
			ATTGTGAAATGGAATCCTATAGACTCAACTTTCGATTGCCCCTGCCATGGTTCAATG
			TTTGATAATCTGGGTCGATGCATCAATGGACCTGCCAAGGCGGACCTATTTCCCGA
			AGATTAACGATAGTTGTTTGTACATGTAATTATCTTGATATTGTATATATATGTATTTA
			AATTATACAGTACAATAAATCCATGTTTGCAGGCTATTTCTGCTTGATAATTTAGCTC
			CAGATTTATACATAACCAGTTTATTTGGCTGTTTTTCCCCTGGCAAAAAAAAAAAA
SEQ ID NO:2	Late	LPS-003	003GGTACTCCACAGAAAGAAATGATTTGACAGAAAAAGAGAGCTGTAGGATTGGGT
			AAACCCTGCAGTGGATATATACAATGTATATGTACTCTGTCTGTTTTTCTGTTATTTG
			ACGGAAATAAAAACGCCATAGCGACGGATGACTGTAAATCCTTAGGGACGGATGAC
			TGTAAATCCTTAGGTTGGAAGATTACAAACGACATATGGGTCTTTCAATTTTCAGAT
			TTCTGTAAGACTTACATTTCAAAGACTGTTTGGATGGGCAAAAAAAAAAAA
SEQ ID NO:3	Middle	LPS-004	GGTACTCCACCAGAATGCCGCAGTTTAGTTCTCTAAAGCAAGCAGTAAATTAATTTT
			GTCAAAATCTAAAGAGTGTATAGTATCAGTGGGTTTGTATTTCCTAGTTTGCCTACA
			ATAACGATGGGGATTCACCAGTTTTTGTAGAATTTGCAATCATCGGATGACAATTTC
			AAAGTTTTCTCTAAGTCACCCGCATTGATATCGAGAAGCCTTCCATTTTCAATTATTT
			AATATCAGAAAATCTTTTCAGTTGGCAAAAAAAAAAAA
SEQ ID NO:4	Middle	LPS-006	AGCCCAGCTGCGAAGGGGATGTGCTGCAAGCGATAAGTGGTAACGCCAGGTTTCC
			AGTCAGACGTGTAAACGACGCCAGTGATGTATACGAATCACTATAGGCGATGGCCT
			TCTAGATGCATGCTCGAGCGCCGCAGTGTGATGAATTGCAGAATCGGCTGGTACT
			CACGGGCTAGAGAAAGGCACAAGCACTTTTTGTCATTTTAGGATCAGAGGCATTCA
			GGTATAGGAAGGGTGGCTCAGATAGGCAGATGGATCGGCATTTTGCCCAGTCATG
			AAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCTTTGTGCCTTCT
			GGTGATATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATATGGTTTGTCACT
			GAATATTTTGTTGCAGATGTTCTCTACTATTTTTTATCTGCTTTCAAGTGATTATTTG
			TTGATTCCCCATGGATAGTTATGCTAATCAGTTGCATTTCTCTTGTACCAGTCAACA
			AACAAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGTAAACGTGTAG
			CTAATTGTTCTGGCAAAAAAAAAAAA
SEQ ID NO:5	Middle	LPS-007	TCCAAAATACAAAGGCTTTATTTGCATCATGATATAATACAAAGTAAGAAATTTACCC
			AACTGTTTAACCTAATAATAATACAAAGGAAGCATTTTACCCAACTCTTTAACGTAAT
			AATACCAAAGAGTGGAATGCTTTATTGACCAGCAAGACCTTGAAATTTTTATAACCA
			ATGCCCATCAACAGAGCCTTTCTTAAAAAACGCAAAGCCCAGCTCTGTCACCTTATT
			AGTTAGTATAAACTGACATTCTTCCAAGCTTGTGTGCGCAGAAACAATAAAGAACTT
			CACCTTGGTTTAAAGAACGTGCCATGAAGAAAACGTCCCAAGAAAAATGAAATGGC
			TCCTTCGACCATTCAGTCCTCCCTAGAAAAATCAAAAGACTCCTTCGACCATTAGGT
			CCTCCAATTGGGCATCTAACTACAAGCGGTC
SEQ ID NO:6	Middle	LPS-008	GGTACTCCACGGGCTAGAGAAAAGGCACAAGCACTTCTTCGTCATTTTAGGGATCA
			GAGGCATTCAGGTATAGGAAGGGGTGGCTCAGATAGGCAGATGGATCGGCATTTT
			GCCCAGTCATGAAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCT
			TTGTGCCTTCTGGTGATATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATAT
			GGTTTGTCACTGAATATTTTGTTGCAGATGTTCTCTACTATTTTTTATCTGCTTTCAA
			GTGATTATTTGTTGATTCCCCATGGATAGTTATGCTAATCAGTTGCATTTCTCTTGTA
			CCAGTCAACAAACAAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGT
			AAACGTGTAGCTAATTGTTCTGGCAAAAAAAAAAA
SEQ ID NO:7	Middle	LPS-010	ACGACGTGTAAACGACGGCCAGTGATTGTATACGACTCACTATAGGGCGATTGGC
			CTTCTAGATGCATGCTCGAGCGGCCGCAGGTGATGGATATCTGCAGAATTCGCTT
			GGTACTCCACGGCTAGAGAAAAGGCACAAGCACTTCTTCGTCATTTTAGGATCAGA
			GGCATTCAGGTATAGGAAGGGTGGTCAGATAGGCAGATGGATCGGCATTTTGCCC
			AGTCATGAAACATTTTATGCATGTTATTGCCTCCCAAGGACGAAATCAGTTCTTTGT
			GCCTTCTGGTGATATCACTTCAAACAAAAGGCAACAGTTCTGTGATTTCATATGGTT
			TGTCACTGAATATTTTGTTGCAGATGTTCTCTACTATTTTTTATCTGCTTTCAAGTGA
			TTATTTGTTGATTCCCCATGGATAGTTATGCTAATCAGTTGCATTTCTCTTGTACCAG
			TCAACAAACAAAAATGCTTGTAGGAATCCATTACTATTTATTTTCAGACAGGTAAAC
			GTGTAGCTAATTGTTCTGGCAAAAAAAAAAA
SEQ ID NO:8	Middle	LPS-011	GGTACTCCACGAAGCAAAAAGAGTCAGGGGAATGAAGATGGGGGGCTCCGACAAG
			AAGCGGATCAGAGAAGAGCAGGAAATGAGTCCACCTGAGGAATCCTGGAGACAGA
			AACAGGGGCGTTTAATGGAGTTTGAGGCAGGGATGGCCTATGATAAACCTGAAAAT
			GCCGGTGCAGGTAATGAGAATTTGCCAGAGTTTTGCTCTCTTTCAAATGAGTACTC
			GATGTTATTGAAAGATCCATGGAGTTGGGAGGATAGCACTGGTTTCGGAATCCGAA
			GCTTAGCTGCTGTCAGGAAGCAGTCTTGTATATTGGACTATCTCCATGATTCTGCT
			GTAGATAATCGCTGTGAAAAGGATTTTGCCGAGCAGCACAAGGTACAGGAAGAGG
			AGGATTGTTTGAGAAGGTCTCTTTTTGAAGCCACAGATGATCAGCTCTGGAGGCTT
			CAGAGTCTTTGCAGGATACAGAAGGTCTGTTTCCTCTGGATTCCGTGGGTAGCCAT
			GATTGCACGACCTTGTTGCAGGATGAGAGCATTGTTCAGGGCGCTGCTTCTTACTT
			CAGAATTTGGGAACAGGATGATGGTCACAAGGATGCCAAAATTCATGAAGATGGCA
			TTGGTTTTGTGTATGGGAGTGGGATCTCGGATTGGATTCGGAGGGCTCCCTCGAA
			TCAATCTGAGTTTTCTGAATCTGTTGAATTTGAAAGCTCTATGTTTTCACTGTAATTT
			GGGTCTTTTTAATTTCTTCCTATGTAATTTGGGTGTTTCTAATTTCTTCCTTCAGCAA
			AAAAAAAAAA
SEQ ID NO:9	Middle	LPS-012	GGTACTCCACCATATCCAGGTAAACAAGGGAAAACAGAGTCAGCTTCTAGTATGTT
			GTATGCCTTGCTCTGTCTGTTTTCTTTGATCTTTGATGCCAAGCAAGTTGAATGTGA
			TCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGTGTCATTA
			GCACAGAAGCTATTGGAGAAATGATTATTATCTGTTTGATAACTTCTAGAGCATTTT

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			TCTGCTTCCAATTCCACAAGGTGGAAAGTGCAAGGATGTTTACTTTCTTAAACTGTA
			CTTGCCTTGTATTTGATGATGTAAGGTTGTGTGGCAAAAAAAAAAAA
SEQ ID NO 10	Middle	LPS-013	GGTACTCACCATATCCGGTAACAAGGGAACAAGTCAGTTTTAGAAAGTGGACCCCC
			GGTTCCGTCGTTTTCTTGATCTCGGAGCCAAGCAAGTGGATGTGATCACTAAATGT
			TGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGGTCATTAGCACAGAAGCTA
			TTGGAGAAATGATTATGGTATTCCACCATATCCAGGTAAACAAGGGAAAACAGAGC
			TCAGCTTCTAGTATGTTGTATGCCCTGCTCTGTCTGTTTTCTTTGATCTTTGATGCC
			AAGCAAGTTGAATGTGATCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTG
			TCTCTTTGGTGTCATTAGCACAGAAGCTATTGGAGAAATGATTATTATCTGTTTGAT
			AACTTCTAGAGCATTTTTCTGCTTCCAATTCCACAAGGTGGAAAGTGCAAGGATGTT
			TACTTTCTTAAACTGTACTTGCCTTGTATTTGATGATGTAAGGTTGTGTGGCAAAAA
			AAAAAAA
SEQ ID NO:11	Middle	LPS-014	GGTACTCCACCATATCCATGTAAACAAGGGAAAACAGAGCTCAGCTTCTAGTATGT
			AGTATGCCCTGCTCTGTCTGTTTTCTTTGATCTTTGATGCCAAGCAAGTTGAATGTG
			ATCACTAAATGTTGCTGGCAGTAGAGCTGGAGATGTGCTGTCTCTTTGGTGTCATT
			AGCACAGAAGCTATTGGAGAAATGATTATTATCTGTTACATAACTTATAGAGCATTTT
			TCTGCTTCCAATTCCACAAGGTGGAAAGTGCAAGGATGTTTACTTTCTTAAACTGTA
			CTTGCCTTGTATTTGATGATGTAAGGTTGTGTGGCAAAAAAAAAAAA
SEQ ID NO:12	Late	LPS-015	GGTACTCCACTAGACCGGGTAGGGTCTCTCCATGGTTTTGCGACTTAGGTTAGGTG
			TCCTGTTCTGTTAATGATTTTGAGGTTTTGTAATTGTGAGTATGTTTCCAGGGTTTT
			GAACCTGGGTACTCGGCCTTTGTTGGAATGTAGTCTGGTTAATTTATATGTATATGT
			AACCTTGGGGTTTCGAGCCCAGTTCTCTGTTCTTCTTGAAATGAAATGCGATTTGTT
			CTAAAAAAAAAAAA
SEQ ID NO:13	Late	LPS-019	ATATATACGTATGGTATTCCACAGCATGAACTCTTCGACATTATATGCTTGTTATAGT
			TTTTAAGAGAGGAGACTTACCTCACACATGTACAGCTTTTTATTGTCGTGCTTTCAG
			TTGATGGATGATTGTTGTAGTCCTGTCATTGGTTGGACAATTTTCATCATCCTAAAG
			ATCCAAGAATTCATGTGGCAAGAAACTTTAATAAAGTCAAATATAATCCGATGACGT
			AACCCTAAAAAAAAAAAA
SEQ ID NO:14	Late	LPS-020	GGTACTCCACTAGTGATCGATTCTCTGTATGTGACGCTGCGCGGCGGCTTATAGC
			GCTTCACTGAGAATGTACGGTATATTATGATTGATGTGATGGATTTGCTCCGCAGC
			TTCGGCTGTTGTATCTGCTCACTTCGGCGTATATATGTAATATGTTGCTTCTTCAGA
			GAGATGAACTTCCCCCTAAAAAAAAAAAA
SEQ ID NO:15	Middle	LPS-023	ATAGATCATTTTAAAGTTTCAGTGATTTGAATCTAATTCCACTGCATTTCCTCGCAAA
			CTGGCAGTCAAATAGTATTCCCTCTTTCAGTGACAGGCTGGCAGGTGTTTCATTCT
			TATACAAACATGATTATCATAATTCCATTAATTCATGGCGTTTTCTTTGCCAAAAAAA
			AAAAA
SEQ ID NO:16	Late	LPS-024	TTTTTTTTTTTTAGGGAGAAAGGTAACTTCAGCCAGCTTTCAAAGGCAACACCTACA
			AAAGGGGTGACTGAGAACTCAGACACAGACGACAAGTGATCATTCGGGCCAGATT
			TTTGTTGAGAGAGTTGTAGTGTGTAATTGATTCATTTCATACATTTGATATGCAAGC
			CTGTACAATAGCCTGTGACTGTTAAGGGCATTCTTTTGTCTCCCTGTTGCTATTTGG
			GTTTCCGGTGTGTTCATTTTCACTTATTTTTGTGTTTTAGCTGGAAGAATTTGAGAG
			GGTAGAATTGTGTCATCGCTATGGCTTGTGCATGACTCATGAGCCAGCAGTTGAAA
			CTTTTATTTATTAAGTTATAATACTATGTCTTGTCAATTCTCAATAAAAGATATTTTAT
			GCTGTTGGGCAGCATCTAAAATGTTTTGTATGTTAGCATAAAATCCCATTTTCTATA
			AGTTTTTGCCAAAAAAAAAA
SEQ ID NO:17	All	LPS-025	AGCAGGTTCAGTCAGACGTGTAAACGACGCCATGATGTATACGAACTCATATAGGG
			CGATTGGCCTTTAGATGCATGTTGACGGCCCGCAGTGTGATATTCGCAGATCGCTT
			TTTTTTTTTTTTTAGGCATGGTGCGCGATGAGCTGATAGCGATGATGAAGACCAAGA
			CCACCAAAGGAAGATTCTTCAGAGCAAAAGCTACGGAGACAGAACCAGAGGACTC
			AAAGCCGGAATCCATTGGTGAGGTACCTGCAAATGTGTGATGGACTAACTAAGAAG
			GCTCCTTGAGAGGACCCATTAAGCACAGTGTTTTTAAGTCCCAAATTCTGTTGCAAT
			TCCGTTGAAAATCATTTTTACGATTTTAGGTATGATGTGTGCAATTTTAAAGTTGGAA
			TTATTGTGGGCAAAGGCTATAAGTGATTGTCTAATCCATTTAATTTATTATCTTTTGA
			CTAAGAGCATATCTAGGCTGGAAGAAATTAGGGCACATTAATGTAAGTTTTGAATTT
			GAACATTCTGGGTTTTGCAATGCAAAACACCACAAATATTTTATAATGTTAGAGGTG
			TACTTTTTCTGGCCAAAAAAAAAAAA
SEQ ID NO:18	Middle	LPS-026	GGTACTCCACCAATAATACTTGTCTGTTCTTGCTTCCCTGCTGATCCACTAAGCAGA
			TTATTTCTGTCCACCCCACTTTAGAGTCTCAGTTTGTAAAGCACTCCCTAGGAGCTA
			AACTCATTTCCAATGGATTAAAGCACTCCATAGGAGCTAAACTCATTTCCAAGGGAT
			TTTTGTCCATTTCTCTGTGCTAAAAAAAAAAAA
SEQ ID NO:19	Early	LPS-027	ATGTATACATATATGTGGTACTCCACACACTCAAATAACAGCATCACAATCAAAACA
			AGAAGGCGGCCAGAAAGCTTTAAAATGCTAAGCCTACAGGTAATATTCACAACTGC
			ATTAAGCACCCCGCTTCCTAGTTCTGAAGAAGCCAGAAAGCTTTAAAATGCTAAGC
			CTACAGGTAATATTCACAACTGCATTAAGCACCCCGCTTCCTAGTAGGCTAGTACTA
			GGACTAGGACCGCATTACCAGTTCCCTTATCTTCTACTCATCCTCTACAGGAAAAAC
			TATGACTAAAACTGCATTACCAGTTCCCTTATCTTCTCAACTCGTCCTCTACAAAAAA
			AAAAAA
SEQ ID NO:20	Early	LPS-028	GGTAATTTCCACCCACCACGGGCTTTTTCAATTAACCCATTTCTACCACTCCACATT
			AGGGTTCTAAGTTTTGTGACTCACCCCCAATTTCGCTGATATTTTGCATTGCAGCTT
			GTTTATCTACAGGAAATGGCTAATCAGTACTTTCAGAATTTGGTTGCTTCTGTACAG
			GAAATGGATAATCAATCAGTACTTCTATACTTAAGTTGCTTACGCGGGGATCAGAG
			CCTTACTTCAGAAAATTGAATACATTTTCTTCTTTGTGTATGTATCAGGCATGGAATT
			ATATGTAGCATGCCATGGAATGCGTATTTACTAGATTATCTTTTAATTTAATACATAT
			GTTGCTTACTAATTTGTCCACAAAAAAAAAAAA
SEQ ID NO:21	Early	LPS-029	GGTACTCCACACACTCAAACAACAGCATCACAATCAAAACAAGAAGGCGGCCAGAA
			AGCTTTAAAATGCTAAGCCTACAGGTAATATTCACAACTGCATTAAGCACCCCGCTT

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			CCTAGTTCTGAAGAAGGCCAGAAAGCTTTAAAATGCTAAGCCTACAGGTAATATTCA
			CAACTGCATTAAGCACCCCGCTTCCTAGTAGGCTAGTACTAGGACTAGGACCGCAT
			TACCAGTTCCCTTATCTTCTACTCATCCTCTACAGGAAAAACTAGGACTAAAACTGC
			ATTACCAGTTCCCTTATCTTCTCAACTCGTCCTCTACAAAAAAAAAAAA
SEQ ID NO:22	Middle	LPS-030	GGTACTCCACTATTAGATTGATGCAAGACCAACTGATCATGGCTAGGGTGTATTCA
			AGCATTTCCCAGGCTAGGAATAATCTTGATTTATACCATGAATTGATGCTTCGTATT
			AAAGAATGTCAACGTACATTGGGTGAGACTAATGCCGATTCTGATCTACCTCAAAG
			GTAATAATTTTTGCATTAGCTGCTTCTAAATCAAGAGTAGTAAGTGCTTCCATTTGC
			AAAAAAAAAAAA
SEQ ID NO:23	Middle	LPS-031	GGTACTCCACAAGGCATATATGGGCAATTGATTTTGCCTAGCCCAAATTCCTATTCA
			AGCTTGCGTATTTCTAAAAGATGCACTATTTTTTGTCCGAGTGTAGGTTTTGAATTC
			ATTGTAACATTCAGCAATATTAATTCAGGGGTAGCATTTCTGGCAAAAAAAAAAAA
SEQ ID NO:24	Middle	LPS-032	TTTTTTTTTTTTTAGGGTAGAAAACCATGCTTCACTAACAAGGTATAAAATTACAATAT
			AATTCTGGGTGTAAACGACCTGATAGATGATCTGCAAGTGCCAGGAGGCAATATCT
			AGCAGAATACGTACAAATTAAATTGCCAAAAAAAAAAA
SEQ ID NO:25	Late	LPS-036	GGTACTCCACCAATGATCACCCATGTCCATTTGGTTAATTCAATGTCAAGATTTAGT
			AGTTCCGTATTCCCTTGGGTAAGCTGTAATGGTCCATTTGGGAACAGTCCATGTTT
			GGGACACAAGTTCAATAGAGATGTCATCCATAAATATGGGTATGAATCTCTTCCTTC
			CCTCTCCGCCCAATAATAAAAAAAAAA
SEQ ID NO:26	Late	LPS-037	TTTTTTTTTTTTAGTAGCAATAGCAATCCATTTTAGGGATCTGCAGATCAGTGACTAA
			GTGACCCCTACCCCCAAAGGATTAATTGTACTTTGGCTTAACCACAAAACCTGATTC
			AAAAAATGTGAAGTTTTTACCCATTAAATTAATTCCCAAAAGTAACTACAAATTCCAG
			AGTACATTTTTACCCAAAAAAAAAAA
SEQ ID NO:27	Middle	LPS-038	GGTACTCCACTATACAATATCAAGGCATATCTGCCGGTTGTTGAATCATTCGGATTC
			TCAAGCACTCTCCGTGCCGCAACTTCTGGCCAGGCTTTCCCTCAATGTGTGTTTGA
			CCACTGGGATATGATGGGATCTGATCCATTGGAACCTGGTTCCCAAGCTGGGCAG
			CTTGTGACTGATATCCGTAAGAGGAAGGGTCTTAAGGAGAGTATGACTCCCTTGTC
			AGAGTTCGAAGACAAGCTGTAGAGCTTTGCTATGTTTGCATGTCGGATGCTGTCAA
			GATTGAGGAACCTCCGAGTATTAAAACACAGTTTTGTGTGCTAGGACTATTTAAATT
			TATGCTATTCACGTATTTTTGTGATCTGTTATTTATGTTATTCACGTATTTTTGATTG
			GAAAATACTTTTTACAAGTCATCCATTAATCTTTTAAATGTTACATAATTCTCTCTTGT
			C
SEQ ID NO:28	Late	LPS-040	AAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTC
			GGCTTGGTACTCCACTATACAACATCAAGGCATATCTG
SEQ ID NO 29	M,L	LPS-041	CTTTTCTTCGTGCTTTTCGTGGAGTACC
SEQ ID NO:30	Middle	LPS-042	GGTACTCCACAAAGTGAGATGAGTGATATGAGGTCAAACACGTAAATGACAATAGC
			TATTATTTCCCCACTTGTTTGTGGCTGTGTATATTATACTTCATTGTCAGGACTTTTG
			TATGGTTGAAGTTGCAAGGTTTTGGCAAAAAAAAAAAAAAA
SEQ ID NO:31	Middle	LPS-043	GGTACTCCACCTCCAGCTGCTTATCCAAGTACTACGGATAGTTCATACTCCTATTAT
			GCTTCTGCCAAGTGAACCAGAAGGCTTCTGTTTCTACACTAGCAAACTGATAGCTC
			GAGCATTCTGATTTACTAAGGATGATAATTCAAAATTGTAACATTGCAAACATCAGC
			AAACATCAGCATCAACTCTGTTACTATTACAAGCAATGGATGCGTCGCTGATGCTG
			CGGGAGAGTAAATTTTTAGTTTACTGCGGTTGGTAATTGAGTAGGTTGACTTACATT
			TCTGTTGTAAAGCCGTTGTCGGGCATTGTTTATCTGGCCGAGTTAGCGCCAGGAAG
			CTAAATGTACCAAATATTTATTTTTATTTTATTAAGAATATAAAATTTAGTCGTCTTCT
			GCTGCCCAAAAAAAAAAAAAAAA
SEQ ID NO:32	Late	LPS-044	ATGGCCATGGACTTATGACTTTCAAAACCCTAAAACCTATCTACAACTTTCCACGCT
			GAGATTTTCCGAGGAAGGCATTCTAAGCCATTCCCACCGTACTTTAATAAAATAAAA
			ACAAGAAGATAGTAAAGCTAAGCTACAACCTTCCGCCAAAAAAAAAAAA
SEQ ID NO:33	Late	LPS-045	GACCGCTTGTAGGAACACTAGCAGATTCCGGAACATAGGTACTTTGAACATCTTTC
			ACTCCTCACCATATGAATAGTGAGTCGATGGCGGCCTTAACAGTCGAGCATGCTTT
			GATTTCGTCTCTCTCTCTAGTGACCGAAATCAATCTCATTATATATGTCATTATGCAT
			TCATTCCCACTTCCTAACTTTCATTATTGTTCAAAACTTCGCCTTCCTGAAAATGCTA
			TAATAGTAGGGGAATATTGAAAAACTTCCGCCAAGCTAAAAAGGCACTTAAAGCAC
			CTGGATTTGAACCAGGATTTCCCACCCCGATGAGGGGGGGTGTCTTTCCATTGAG
			ACGATGCCTTACTCGGCAGACCCTGTGGGGGTCTTTATAGGTGACTTAATACTTAA
			GTATAGGACTTAAGAGAGAGGAAGCGACCGCCTCTCTGATCAAGCCTTTACGTGC
			GACGTGCCCAGGTAAAGGCTGATCTCACCAAATAATTCAGAGAAAGAAGATGACTC
			CACAGTAGCGAAACTCCTACATTGTCTTACATATCGTAACAAGCGGTC
SEQ ID NO:34	Middle	LPS-046	GACCGCTTGTGCCTGGTGTCCAAACTAGGACGCCTTAGTTTTCCTAAGAAGGAAAC
			CCAGGCGTTGACTTGAGGCAGACTTGTGCTTCTGGGTACTCTCATTCACTGCGTGA
			CCTTGAGAAAGGGACTTTACCTCCAGGATCCTCAAACTTCTTCTCTGTAAAATGAGC
			ATTGTAATAATTATATCCCAGGCTTATGTTGGGAATATTCAATAAATGCTCCCTTCAT
			TCTTTAAAAAATAAGTAAAGACAGCCTGAATGGGAGCCACGTTCTCATTCTTCTTTC
			TCTATGCAAAATGTATTGTGTAATGTTTGTGTACTAGTAGTTCAAGAGCAAATAAGT
			AGTTGGTTAATGGCTAACATATTTCTTAAATTTGTAACTGTTAAGATAAACATTGAAC
			AAGGAAAAAGATTCGTAACTGAAATGTAAAGTCATTTGACCCTGGATAGTCAATGAC
			AATCTTATTCACAGTGTAATAAGTAATTCATAACGAGATGATTATTATGAAATTATCA
			ATAGCCTGCTATATCACTTTATGTTTATGATCCACAAGCGGTC
SEQ ID NO:35	All	LPS-047	GACCGCTTGTGGAAGAAAAGAAAGAATCTCTTTCGGATTCAATAGGCGGTATGGGA
			GAGTCTGCTACTGCCTCTTGGATTCCAGGAATCCTAGAGCTGGGAGTATGAGTTGG
			AGATGATGAAGGTGTCTCTTACCTATTTCTTGAAGTGGATGGAGTTGTGAAAATCGA
			ACTTCTAGCTTCAGCTAAAAACCTTCCCCTAGAATCTCTTGCTCTATGCATATCATTT
			TTATTTTTTCTTTCAAGATAGGGTAATAATTCTCTTTCTGATCTTCCAGGTCACTCTA
			GGTGCAAGAAGAGAGCATAGTCAAGGAACTATTAAACCAATAACTTTCTCTTTTCTG
			ATCCTCCAGTTCACTCTAGGTACAAGCGGTC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:36	All	LPS-050	GACCGCTTGTGCAAAGTAGATACCGTCCTGTTCCGGTGAATTGAAGTACATTTTCA AAATGCGCTACTATGACATTTTATAGGATGTCTGAGTGTAAAATAATGGTACTGGTT GTTGCAAAGAATCTGATGTTTGGATGTATGGAACTATAAATAGATGTTATTTTCTGA TCCAGAAGGCTTTCCTTACCAACTGATTTCATCTTCAGAAACTAAAAGCTCTTGAAC TTGTGTAGATGGGGCTTGGTCATTGTAGTTTAAATGCATTATGTAGTGGCAAAAAAA AAAAGTTATAGCCTACGTTTCAAATGGATTTGCTCGACAATCAAATGAATTACAATT GAATATTCATGTATACCCAAATTTTAAATGTAGAATGACATCATCAATGTAGACAAAC ACCACTGTGCTTGTCCTTGATATCCTCTTTCACCATATAATTGGTGGCTTACTCAAA GTCACTATCTGATGCAACTACAAGCGGTC
SEQ ID NO:37	Late	LPS-051	GACCGCTTGTTCAATGCAGAATCTCGAAGAGATGTCTTGGACAAATACTGAACTGG CACGATTGGTGTAGTGCGGTTCAAAAGGCGCTCCAGATTCGTCTGGAACGAATCTT CATACGCTGAACAATTAGACATCTTGTACGCAAGAGAATTACGATCGGCCATATAAA AACCCCAAAGAGAAGAAAGTGTTTCGAAATTCTCCCAGAAAACAGTCTTATGCCAC CGATTTGTCTTTTCAACATGCATTTGCAATGAAGTCTTTGGATTCTTACTGTGAGTG CTGATCAGCAACGGATTTTCGATCTGTATAGCTCTGCCGATTCCTGGTTAAAGCAG CTAAGAGTTAGGCATCCAGATTTTGAGTTTTTTGCATCTCACAATGTTTGAATACATT TCAAATCCATTGTTGGAGTAACCTAACAACAACTGTACTCTTCTTCCTATTTCTGAA GCCCTCTGCCAGTTTAAGGCAGAGAACTGAGTTATCTACAAGCGGTC
SEQ ID NO:38	Late	LPS-052	GACCGCTTGTATAATAAAGTGGTACCGCGTCCTGCAAACAGGGTTCTCTTGCCATC CTGCTACAACCCTGCAGTGGTCGCAGTAGAGAGAATCGGAGCAACGAACGTTTTC CCGAATATATGGAGCGGGAGGAAGAGTTTTCTTGCTGATGATCCAATCGGAGTCGA ACTGCCACCGCTGGATGAAGGGCGGCGAGGAAATCTTGGGGGGCAGAGGCCCGT CGGCGTAGGAAATAAGAAACGATTTGATATGGAACGAAAGGGCCCGTCCAGGGTT CGATCCCCGGCAGGGCAGCCAGCCCCGAACTAAACAAAACAATAAGAACAAACAG CAAAGTAAAAGAAAGCACCAGAAGAAACAGCAGCAGACGAAGAGTAAGGAGCTGC CCACAAGCGGTC
SEQ ID NO:39	All	LPS-053	GACCGCTTGTAATCCACAGCATTTTCAATAACTTCCTGAGGTGACATCCACCTCCAC TCAGAAAACTCGGCTGCATCTGTCCCATCACCAGCTAGATTGATCTCACTCTCGTC TCCTCTAAATTTTAGGAGGAACCATTTCTGTGCTTGACCTTTCCATTCGCCTCCCCA CAAGCGGTC
SEQ ID NO:40	Middle	LPS-054	GACCGCTTGTATATAATGTGAAGACACAATAAAATTTTGTCCAACAAAGCAACCAAA CGACCAAAAATTTAGCTGTGACATCAAAAAGCTCAACCCCTACAATGAATGTAACCT TAATCTAGAAAATTGATCCATGATCTCCACTGAATTTTCTCGTTCATCCTGAAGAAT GAGAAACTTAAATGTACCCGATTCCCTCAACCAAGCCCCCACAAGCGGTC
SEQ ID NO:41	Early	LPS-055	GACCGCTTGTAATCCACAGCATTTTCAATAACTTCCTGAGGTGACATCCACCTCCAC TCAGAAAACTCGGCTGCATCTGTCCCATCACCAGCTAGATTGATCTCACTCTCGTC TCCTCTAAATTTTAGGAGGAACCTGTAATTGGTAGGGGCTTGTCATAAATGATCAAG ACGACCCGCATCGTGATGCCAAGCTTAGTCTTTCTACTTACTGTCTATGTAATGGTC ACGGGCCCTTCTTATGTTTATGTCTCTTTGAAATGGACGATTTTTTTGTTTTAGGTAT TCAGTTTCTGAAGCTGTTTTGGTAGTAAACTGGGCTCAATCATTTCTGTTGCTTGAA CTTTCCATTCGCCTCCCCCACAAGCGTCAGCCGAATTCTGCAGATATCCATCACCT GGGGGGGCCGCTCGAACATGCATCTAGAAGGCCAATCCCCTATATGAATTCTATTA AATCCCTGGCCTCGTTTTA
SEQ ID NO:42	Early	LPS-056	GGTGCGATCCAGAAAACTATCATCTCTCACTGCTCGTGAACAAAATGCTGGTTCAT AGCCATCACTAAGGCTAAGGTACTATCCAGCCAAACTGATCTCAAATAATAATTTCA TAAGCTTAAATAAATAGTCCAGCCAGTAGATGGAGCCAAAAAGCCATAGAAGCTTC AAATACTTGTGGTATCAATCTCTCCTCTGTTAAGGGAGGTATCAGATCAGAAGCACT AATCAAATGCATACATAAATGCAGTAGACTGCAATAAAACAAAATCTGCAGATAGCA ACAGAGCGCTTAACGAACGGAAAAGAGTTTAACTTGATCTATCACAGGATCGCACC
SEQ ID NO:43	All	LPS-057	GGTGCGATCCACAATAGTTCGTACGAGCGACGTCTATCTGGTTAATCAGAACACAT ATCTAATTTGGAAATTTGTGGGCATAAAGCTCCACAGTGTAGGTGGGCTAATCCCA TGAAACATTACTCTTCAAAACATCATACAACTGAGGTGGAAATTGCAAAAGATTATT ACTGGATGCTGATCTGGGACTAAGGTGGTGGCCATTGGTAATGTTGTGTTTCAGAA ATATATCTTCATGATGATCAGTAGTTGCATCTGGTTGGAAGAATGATAAATTCTGGT AATTTGTCTTGGGATCGCACC
SEQ ID NO:44	Late	LPS-058	GGTGCGATCCAACTAGAAGAATATAAAGAAAAATTACGGACTACCAGAAAACATCA CATCACAGTGTATTGCATTCTCAATAATCAGAACTGTACTGGCTAATATCGCTGTGC CTGTCGTTTCATTTTCCTGTCATCCGCATAGGGCCCCTCATTTTCCCTATCTTGCAG AAATCCAAGAAATGCAAGAAAACCAAAAAGGAAGAAACCCCCAGAGGAAGAGTCCG AAGAGGATATGGGTGTCAGTCTTTTTGACTAGATTGGAGGATCGCACC
SEQ ID NO:45	Early	LPS-059	GGTGCGATCCCAGAACATTTCAGACAGATTAAAACAAGATCTAGTCAATTCCTACAA GGGAAACTTTTGTCAAGATCCGGATCCAGATTTTCCTCAAGTAAAACTAATCTCATT AAATCCAAGCCAATCTCTAGCAAAATTCAAACACTTTTTATTAAATCCAAGCCATATA TCTGGCAAATTCACCGAAATATGTACAATCGCAGCGCATTGCTTGGCTTGCGACAG AAACCATATTCGCACGTCTTCATAAGGCTTTGGATCGCACC
SEQ ID NO:46	All	LPS-060	GGTGCGATCCAACAACACAGCTTCACACTTACTCCATCCTCTGGAACTCTCATCAG ATTGTGTTCTTCGTAGACCAAGTTCCTGTGAGAGTCCACAGGCACACTGAGGCTAC AAGCGATGTGTTCCCTAAAGAACAGGGGATGTACATGTTTTCCAGCATTTGGAATG CAGACGACTGGGCAACCAGGGGTGGGCTTGGGAAGACAAACTGGACTGCCGCTC CATTCAGCGGATCGCACC
SEQ ID NO:47	All	LPS-061	GGTGCGATCCCAACACCAAGTGAGAATGAAGCAATATAAATCAGCAGACTCACTAA AGCCAAAACAGTGAAAAATGTTTCATATTGGGAATCTGCTCCAGAATGAGCCTTCAA GTAAAATGACAAACTAACGAGGAAGAGACATACGGCCATGCCCCCAGATGAGACC ATGAGGAGGAGACGTCGTCCGGCTTTATCCATGAGCCATACAGCAACTGCAGTCAT GATGACCTGGATCGCACC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
ksSEQ ID NO:48	Late	LPS-062	GGTGCGATCCAGGAAATCATCAAAGGGGAGCACATCCAATGTGCAAAATAAGATCA TCATGCAGCAAGATCTCTGAAATATAAGCTCTGTAAGACCAATCTGAAGTGCTGATG ATCAATATGAACTGAAACATCATGCCACAATGGGCTGGTACTTGTGCAAAATTCTCT GGCATGTGATGAGAATCACATGGTTACCTCTTTGGATCGCACC
SEQ ID NO:49	Early	LPS-063	GGTGCGATCCAAAGAGCCTTCTTGCAGACAATCCGTGAAAACATGGCTATACAATA AATTCCCAGTTTGGAATTCTAAATAAAACTGTTCAATATTTGAAGGCCTCTGATATCA CAGAGACTGATATTAGAATGGAAGCATGTAGCAACCCTAGAAGCTTTCGCATAAAG ATACCAGATTAATTCATAAGAAGGATCTCTCGTTCACCAGTCACATATCACAGTCGG ATCGCACC
SEQ ID NO:50	Late	LPS-064	GGTGCGATCCGTTAGATGAGCTGCCAAGTATGGAATTATTGACATTTTTGGACGGG TTATGGGCAGAGGGATGTGCCAAGCTGAAGAAGATACCGGGGTTGGAGCAAGCCA CAAAACTTCGAGAGTTAGATGTTAGTGGGTGCCCTCAGTTAGATGAGCTGCCAAGT ATGGAATTATTGACATCTTTGGACGGCTTGTGGGCAAAGGGATCGCACC
SEQ ID NO:51	Middle	LPS-065	GGTGCGATCCACATAGTTTGAATGCAAGGAAATTGCACATACTTCGTGGGGAATTT CGATGGCAAATCAGTCCAGGTAAATGACTTCTCAACATAGGTCCAAAACTCTTTCAT AGACCAGATCTTGACCGTGTTGTCCATGCCACAGCTTGCAATACGATATACATCTG AAGGATGAAAATCTACACTGAGAACTTCATTGCGATGTCCCCCAGCTCCAGCAAAT ATCAAAATGCATATTCCAGTTTGAACATTCCAGAGTCGTACAGATTCATCTTTGCTA GCAGATAAAATAAGGGAAGGTTTCAGTTGCTTGGGTCCTTATTTCATTCACAGAACT CCATGGCCAACGAAACTCTTATGGACTTTTCATTTGCACATCCATTCTCGAATTATA CATTGTGACCGCAGCCACTAATAATGGGGAACATCACTCGCCTGCCCACTTATGTG TTAAAGAATC
SEQ ID NO:52	Late	LPS-066	GGTGCGATCCCCTCCATTTACCATGGTATACTGTTCCAAAGGTTCCAGAGCCTAGC TCTTTCAATTCTTCAAGGTCAGCATTCTTTATTATCTGGAAACTTCGCTAGCTGTGT CTATAATCACGAAACCCAGACGGGGAACTAATAGGCGATGAAGTTTCTCTTATCCA TAACCGTTGCAAAGATCTTACACGGAGTTTTCTCTTCTTCTGCGTGGCTTTTCTTTC CCGTATTCTCGGATCGCACC
SEQ ID NO:53	Late	LPS-067	GGTGCGATCCATACATGCGAGGGCGCATGAGAGACTACCACAAATCCTACATACCT CCATTCACCCCTGGATCGGTTATACAAGGATTTGGGGTGGCTAAAGTGATACTCTC AAATCACCCAGACTTCAGAGAGGGTGACTTTGTATCTGGTACTATAGGATGGGAAG AGTACAGCATAATACCAAAAGGGAGTAACTTAAGAAAGATCAAATATACGGACGTAC CACTTTCATATTTTGTGGGTGTTTTAAGAATGCCCGGGTTTACTGCTTATGCTGGAT TCTTTGAAGTTTGCTCTCCTAAAAAGGGGGAGCATGTTTTTGTCTCTGCCGCTTCA GGAGCTGTTGGCCAGCTTGTTGGGCACTTTGCAAAGTTGATGGGTTGCTATGTTGT TAGGGAGCGCGGGTAACAAACAGAAGGCTGATCTGCTGAAACATAAAATGGGCTTT GATGATGATCTCCACCATAACGAGGAGCATGACTTCGATGTGGCTTTAAAAAGGCA TTTTCCAGATGGGATTGCACC
SEQ ID NO:54	Late	LPS-069	GGTGCGATCGAACTGAATGAATGACGTTGCCAAGCTATGTTTGGGAATTAAAACTT GAATGCCGTTATTCTCTCCTTTTTCCAAAAGGGCCTTTTCTGCCAGAAAACCTTAAA TTTCTGACTGGTTTCCAAGTCCAATTTTTAAAATATGGATTGGTTTACCATTGAAGG CACCACCATGCTCTGAAAGTTATGGACTGCACTTGCCCCAGTGCTATATTTAGTCC AGATAGCGCTTGTGTCTCTAAATGCATCTCCCTGCTCGGATATCACC
SEQ ID NO:55	Late	LPS-070	GGTGCGATCCGAACAGAGGGAGCAGATTTTGCCCTTGCAAGTATTCACAACATTAG AGAAGCCCTGCCAGAGATATGGGAGGAAGAAGATGCAGAGAACACCAAAAATGTT GTGGGATCAAGAGGAGCGGATGCAACTATAGAAACTGTTGTCACGGCATAAGCCA TCGCCTCATTGAATGAGGGAATGGAGGACTAGACAAATCCCTTTGGATCGCACC
SEQ ID NO:56	Middle	LPS-071	GGTGCGATCCGATTGGGCAGCTGCAGCCTTGGGAAGCTTTAGAATCAAATTGCAC TCATCCTCCAGGAGGTATTGAGAAGTCAATTTCTCAAGGTCTACAGTGACAGAAGG AACCATCTTGACAATCTTATCAGGTTTCCTGCTCTGGTTAAACACTTCAACTTTGAC AGGACGAGAGAATGTGACTAATTCATCTTCTTCATCAGACTCTACATCTTCCTGTTT CAAGAAACAAAGATACTGATCATCACTAGGGCAAGAATTGATGATTTTGATATCTCT GGAGAAGCCAGTGTTTACATTGGTTTGCTTCATGGCCACCAGTCTATGGCATAAAG CTTTCCCGAAAGGGTACTTGGCAGATTTAACAGAGCCCAACGTTATATTTAAGGCC CATCTCTTTGCTCTCAAAATTTTTCTTGCATCCTCTGGAGAATATAAAACCCCTTGG TGTCTCTTTCCACAAACACCTTCTCATTGATC
SEQ ID NO:57	Late	LPS-072	GGTGCGATCCAACTGAGAAGGGTGTTTGGTGGAAAGATGACACCAAGTGGGTTCT ATATTCTCCAGAGGATGCAAGAAAAATTTTGAGAGAAAGAAGATGGGCCCTTAAATA TAACGTGGGGTTCTGTTAAATCTGCCAAGTACCCTTCAGGAAAGTTTATGCCATAG ACTTGGTGGCCATGAAGCAAACCAATGTAAACACTGGTTCTCCAGAGATATCAAAA TCATCAATTCTTGCCCTAGTGATGATCAGGAAGATGTAGAGTCTGATGAAGAAGAT GAATTAGTCACATTCTCTCGTCCTGTCAAAGTTGAAGTGCTTAACCAGAGCAGGAA ACCTGATAAGATTGTCAAGATGGTTCCTTCTGTCACTGTAGACCTTGAGAAATTGAC TTCTCAATACCTCCTGGAGGATGAGTGCAATTTGATTCTAAAGCTTCCCAAGGCTG CAGCTGCCCAATCGGATCGCACC
SEQ ID NO:58	Late	LPS-073	GGTGCGATCCATGTAGTGCCAACTTACGAGATCACTAACTTTAAAACTATCATGCAA TTGGCCAATAGAAGCGACACTTGCTGTGCCAAAGTATCGATAGGCTACTCCCGATG GCTCAATCATATATAGTTGGGGCCCATCTCTATCATAACCTCCAAGGATAACTCCAG ATCCAAAAGGCCTTAACCACCAATATAGTGTGCACAAATGCACATAACTGGCAACA CGTTCACAAAGTTCCTTAAT
SEQ ID NO:59	All	LPS-074	GGTGCGATCCCATGGGATAGTTGCAAGACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTAGCAAAATTCAAACACTTTTTATTAAATCCAAGCCATATATCTGGCAAATTCACCG AAATATGTACAATCGCAGCGCATTGCTTGGCTTGCGACAGAAACCATATTCGCACG TCTTCATAAGGCTTTGGATCGCACC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:60	Early	LPS-075	GGTGCGATCCCACTGTAGTTGTCCTTGTTGAGCATAGTTCAAGCTGTTCTGATTCC ACCAGTTAGTGGCCCAACACTGCGAGGTGCTGCCATTTCCATTCCATTCACAGACG TCAGTGTTGAAATTCATATAGGAAGCCACAAAGGGTGAGGAAGACCAATCTATTTTC ACTCGCCCCCCTTGAGTTGCCCACTGGTCTCCGCTCCATATGCTAGAGAATACTCT CATTGCCTGCTCATTCGGATAGGGAACGCCTATGTTTTCATTGTTTGCAAATACTCT GATTGGCAAACCATCAACGAAAATCGCAATTTGCTGGGGGTTCCAGAGAATAGAGT AATTGTGGAAATCTGCTGTAGGATCGCACC
SEQ ID NO:61	Early	LPS-076	GGTGCGATCCCACACTCCTAACCCTATTATATGTCTCCCGTCCATGGAGTCATAGA AGGAGTACGATAATATGCCCTTCAGCCAAGCGAAGTATGACTTTAGTATGGCCAGG CAGCAGTATGAAAGCACATCTTGTTTCTTCCAGGTCGGCATGTATAGTCTCCGGAG GCTAACAATGTCACCCAAAGCTAATTGCGCAAACGGAACTCCTCTGCTGATCTCCC GGGAACTTAGGCGGAACCACCCTGAATCCACTATTCTCACCGCGCATTTCATCCCT TTGGTGAACGCCGCTGCCTCTGGTAGATACAGAGCTGGCTTGTCTCCACTGGAAC CCCCTTTCCGGATCGCACC
SEQ ID NO:62	All	LPS-077	GGTGCGATCCAAACTGTGGTTATCGGTGGAGAGATTAAGCAATTTATTGGAGTAGC AAGTACGCTGAATTAAGGGGGTCCATCTTCAAGCAAAGGTTCCTTTGGATGACTAT GTGTTCTGGAAGTGTTTATGGATCAATCATCTCATAAATTTTGGTAATATATAACAGA AGATTATGGCATCCAGTTAGGATGGTAGTTTCATTGAGGTATAGTAAAAACTACACT AGTCTTGTGTTGCCACCCACTTTTCAGAGAAGTCAGGAGGTCTCTTTGTGAATCATT GATAACTTTATGAGTGGGTACCTAAATGAAATATTTGCATCTTGAGTATATACTCAAT TGATCTTACTTGTGGATCGCAC
SEQ ID NO:63	Middle	LPS-078	CTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTTACG GCTGCGAGAAGACGACAGAACACCTATCATAACTTGAATTCTGATGCAAATCGGAA TTTGCCAAAAACTTGGACGGAAATATAATAGGCAATATCATCCCCGCAAGTAACAAA AAAATTGCATGAAAGCTCAAATCCTATGTGCTTTACACCTTGACTGCATACTTTCTC ATTGGAAAATACATCTCTTTCTTTTTCTGTCTCTCAGTCTTCAATGACGCCTGATGCT TGGTAAGGCGTCGCCTGATAGCACGAGTCTTCTTGGGACGCAAATCAAGAGGCAG GTACTTCTTTTTTTTGTATGCTTCTCTTAATGCGGATCGCACC
SEQ ID NO:64	Late	LPS-079	GGTGCGATCCAAGATTGTACGGCACAGGCAAATGCTGTTCTTTTTCTTAATCACGA TGTGCTTGAAGAATATGAGCGCCGATGTGAACAGATCCACAACCTGGAGTTAAAAT TGGAGGAAGACAGAGCAGTGCTGAATAGGAGCTTGGCAGAAATAAATAGTCTTAAG GAATCCTGGCTTCCCACATTGAGGAGTTTGGTTACCAGAATTAATGAAACTTTCAGC CACAACTTTCAAGGGATGGCTGTTGCTGGAGAAGTTACACTAGATGAACATGGCAT GGATTTTGACAAGTTATGGTATTCTAATAAAAGTCAAGTTCAGGCAAACTGGACAGT TGCAGGTATTGAATTGCTCATCATCAGTCTGGAGGGATCGCACC
SEQ ID NO:65	All	LPS-080	GGTGCGATCCGAGGGAAGCGATGTAGTCTTGCCCCAAGCGACGACCATGATCCCT TATTCTTGGGCAATATGTGCAAGACGTGGACAAATGAAGCGGTTAAAGGGAAGCTT ATGGACTATGGAATAGAGGGTCTTGAAGAGCTAACTCTAGTGGGTGATACTCAAAA TGAAGGAATAAGCCGTGGTTTTGCATTTATAGCATTTTCTACGCACATGGATGCGAT GAATGCATACAAACGCCTTCAGAGGCCAGATGTTATTTTTGGTGCTGATCGAACTG CGAATGTGGCATTTGCAGAGCCACTGCGTGAGCCTGACGAAGAGATCATGGCCCA GGTTAAGTCAGTGTTGTTGATGGGATCGCACC
SEQ ID NO:66	Late	LPS-081	GGTGCGATCCAGTCCTGAAAATGTACTTTACCATTTGTATAATGATGTAAAAATCTT GGCCATAGTCTGGTCAAACCAGACTGTATTGTTGCTAAAGTTATGGAAATTCTGGC CATATTTTTGTCTAACCAGACTGTATTGTTGCCAAAGTTATGGGAATTCCGGCTATA TTTTTGTCTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGATCATAGGG TTGTCTGTGCGTGTCTCTCTTCTTACACAACAAATTTGTGTGTTTTGCAACTATCCC ATGGGATCGCACC
SEQ ID NO:67	Early	LPS-083	GGTGCGATCCGCTGGAAGGTGGGCAGCTGGACATCTGGGAATTATAAGTCGAATG TCAATTGCTGGGCCATCTGGGGGATGAGCAATAGCATCGGAGGCCAAGTTCTTCT GCAGCCGGGCACCAAATGCCATGTGGAGGTCTGAATCTTAGTTTGGAGGTCGAAG TTTCAATCCCCTTGTGTTTACTCTGTTTCTGGTTTTATTTGAATAATTTGAGCAATTT AATGTGGGTCCTTAGTGCTTCTGTGGATCAGATTCTAGGGAACGCCATCCTGATAA GTAAAGATCCGAGTTTTAATGGAGATTCAATTCTATCAGAATTCCATGGTGGTTTAA ATTCCCTTGTACTGTTGATCTACGTCGCTTTGTATATCAGTGTGTGTTAAGATTTTCT CAGAATCCACAGCTTTGTTATGGATCGCACC
SEQ ID NO:68	Middle	LPS-084	GGTGCGATCCAAGCACTTACGACTCCCAACAAGGACGGGAAACTCTAAAATCGGAA AAATATCATATACTGAGGCATCAACTTTGTTGATAAAACTTTAAACAAGAACAATATT TGCAGCATATTAGCCCACATGCCATAATGACAAACAAATATGAGAACACTGCCTACA GGTTTGCCAAAAGCATGGCCCTCACTTTTGCCCTGAGGTCATCAGGAGCTTCTGAG GCTCGAGAAGGAGAAAAAGATTGTGTCACTTCAGGAGCTGAGGCCTCCACATCTTT TAATGATTTCGCAGCAGGCCTCTCTTTAATGTTTTCTTTAGAGGATCGCACC
SEQ ID NO:69	Early	LPS-086	GGTGCGATCCAAGGTACGAGCGAACAAGTTTCTTCAGCAAGCCACCTGGAACTTTC CATGAGTCCAAAACAAGTTGAAGAAGGCTTCTTTGGCTACTTTTAAGATGCTGAAGT GATTGTGCTCGCCTCTTGCACAGTTCAACCGCAATAACATTGGGTTTTACAAAACC GATTACCTGTTTAACCTGCTGTGCACTCTTTTTCGAAACATGACAAGTTCCAACAAG ATAAACTTCGGCCCCATTCTCGCCATTCCGCAAATAAACCACGCTCTCATCTTCTGT TATCGAACTCGAGTGCATGCCACGACGCTCAATTGCAGGATTCCAACCCCGGACTT GCGAATGGTGCAAAGCGATGCCCGTTCGTCTCAGCGATACTGCTAAAGATCGGCA GACCCGAACCAGTTTGATGCTTCCATTGCCTTAAACATCCAGAGTTTTCCTTCGACC TTAAACCCTAACAAGATTACTGATTTCTGGTCCGGATGTTCACTGTCTGTTATACTT CTCACAAATCTGTCACACTCCTGATAATCTTCGGTATTGAACTTCATTGAATTGAATT TTCCTTCTCATTGGAATTCAATTGTACCTTGTAAATGTCTGGATCCTACACTATACCA ATATTTACAGGTCTGAGTATTTTGCCTGTAGTATAATTATCTTTCCTTCGGTCTCGT GTTTCCGTATTATTCGTGTAGGATCGCACC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:70	Late	LPS-087	GGTGCGATCCCGGGGGGAGGTTGATGTTCTGAGAGAATCAATGAAGGGATTTCAG CTGAGCTTGCCTTTTTGAAGACGGAATGCGAACAACCAGTCATTTGCAATAGCGAG AATTCTCTTAAGCCACTGCCTGCTGGGGAGGCGAGTTCTGATTCCGGTGATTGCAT CACTCAACGGCAGCAGCAGCGGCAGAACCTTTAGTTTCCCATGACAGGTCTCTCTG TACAAGTATCTTCCTGTTATGATCTAATTCCGGGTTGTTCGATTATCGTGATGTCTC CTGTATTGACATATTAGCAGAATATTACCATGATACGATGTTAAGTGGCATGGTTTA TGCCCTGCATGTTATGTTATGGAGGAGGTGAGGCATGTGGCGCTCATGGGAGGGC CCACATGGTCCATGGACGTCTTATTAAACGCATAGTCGTGAATGAAAATAGTTCAAT ACATTCAAAATTCCAACACAATTTCATTACAATGGAAGTGACTTCGACTTGAATGTT CATTGAAGCATTTGCATGCACAAACAAAGTATACTAGATTAGAAGAAAATTGCAAAA AAGGACATTGTGCCCTTCTTAGTGAATATATAAAGATGTTCTTCATGCTGGATCGCA CC
SEQ ID NO:71	Middle	LPS-088	GGTGCGATCCCAATAGCCAATATTGCCTCCAAGATAGCCTAGACTGCCTTTTGCAT AGTTCTAGAAGCCAGTCACCCAACCTCCCAAAAGAAATTGCGCAATCTTTCCCATC AGTTTCCCGGGTATGTGTTCTGTCATTCCCCGAATTTTCTTTGGTTTTCACTAATAG ATTTCTTTCCATGCACATTGCTTGTCTCCAGATCTTTTAGGTGTTCATCCATCTCTTA GTAGTACTAGATCGATGGCTTCCAAGAGAACAGGATCATATGACACTGTTGGAAAT GTAGCTGGAGCAGCAGTTGAGCAAGTGTCCTCTAGTCTATCTATCTATGAAAGATA CACATTGTTTCTAGACATGGATATCAAATTGAAATTGCGAGAAGTCCATGAAACATT TGCCGCCTTTTGAAGAAAGGCTCCAAACTGTCAGGGTTCGTTGAACATCACATGTT CTCGCTGTCTGATCCCCCC
SEQ ID NO:72	Middle	LPS-089	GGTGCGATCCTCAGGGTAATGGCCTGGCTGAATCAAGTAACAAGAATCTTATAACC ATTATCTAAGAAGATAGTAGGAGATAACAAGCGGTCTTGGGACAACAAAATCAAGT GCGCTTTGTGGGCAGATAGGATAACTAAAAAGAAAGCCACTGGTAAAAGTCCCTTT GAACTTGTCTATGGCATGGATTTGACATTACATGCCCATCTTAAATTACTAGCTTAC CAACTCCTTCAACATTTTTCTAGTGATAAAGGTGTTGTCCAAAACATGGTTGATCAA ATTGTGCAGTTGGATGAAATCCGCAGGAAAGATTTTGATAGTGCAAAAATCAGTCTA CCATTAAGAAAATCTTTGACAAATCTTCTCGGTCTAGATATTTACAGGTTGGAGATA TGGTTTTACTATGGATTCCACC
SEQ ID NO:73	Late	LPS-090	GGTGCGATCCTGCAGGCTTAGATAGTTTCGGCGCTCCTCTGAAAGAAGCACGAGT AGGTGTCTCCACATTAGGTTGGCCTGATCCCTTGCCTGCACTTGCAGCTTGTCTTA CAACATCTCCTATGCTTTGATCCAGGCTTTTCACTGACATAACTTCAGGGGCTTCCT TCTCCCAGGGCCGTGCTGCCATCCAGCGTTCTAGCCAGCTCCATCCCCAATTTGG CTTGTTTGGGTCAATTTCCATCAGCATAGGATGAGCTGCTCCTCGTGTGCTTTTCAA TGACTGATGAGAATATGCGTTATGCCAATGCCCTTTCTCGCTTCATGGCTGCTTCTT GCTTGCTTTGCAAACTAGCCTCAATTTCCTCTTTGGATTGCAACTGTCATCCAATCC TTTGCTTCCATACTGGATCCAC
SEQ ID NO.74	Late	LPS-091	GGTGCGATCCCAAATGAACATTCAACATTCGATCATGTCAAGCGCTAAATGCCTTG GCAGCTTAAAAGCTAGACTCCGCAAGTGACCCTTCTGACTTAGTACACATATTAAGA CTCATCAAGGGTCCAATTCCATGAAAAGAAATTTTAAAACGGTTACATATTCACAAG AACAGCACGAGATTTCCCAGATAGTCAACCACCAACTTGCCCTATCAGCCCAAATA TTACTCATTCCATGTTAAAAATAGCAAATTTCCAGATAGAATGTCGAAAGAGATCTT CATGCACCATATATGGACTCTTAAAACCAGCCAAAATCTATACTGCCATGCTTGGAT GGCACC
SEQ ID NO:75	Late	LPS-092	GGTGCGATCCTGGAGAGAGAAGCAAAAAGCCTACCATCTAAATCTACATTCTAAAT CAGATATCTTTACTGTGAAAGGAATTGAATGCTGCTTCAGATATCCTACAAGAATTA AGAAGAAAAGAATGATCAACTCCAAATCAGGCAGATGGCTCAGAATTTCCCGCAGC TTCATTTTCGACGGCCTCCACAACACCAACCTCGGCAGGACGTATTACTCTGCCAT GAAGTGTATAGCCAGGCTTCAAAACCACAGCCACACTGCCAGGCTGCTTACTAGCA TCTTGAACTTGAGATACTGCCATGTTGCATATGAGGATCAAACTCTTCATTTATTGG ATCGCACC
SEQ ID NO:76	Late	LPS-093	GGTGCGATCCCCAGAGGTTATTTTGGGTTCAAAGTATTCTACACCAGTTGACATGT GGTCATTTGCTTGCATAATTTTTGAACTGGCTACAGGTGATATGTTATTTGATCCTC AGAGTGCAGAAGGTTATGACCGCGATGAGGACCACCTTGCCCTGATGATGGAGCT TCTTGGAAAAATACCTCGTAAGATCGCCTTAGGTGGGAGCTATTCACGGGAACTTT TTGACAGGCATGGGGATTTAAAGCACATTAGACGGCTTCGGTATTGGCCCTTGGAT CGCACC
SEQ ID NO:77	Late	LPS-094	GGTGCGATGCTAAACTGTATGTCTCCACAATTGTCTTCAATATAGAAGCAGCTACG CCCCTCCTAAGTCATCATAAGTTAAAAACTTCATCTTTCCAATACAATTAAACTATCT AGCTTATCAGTTTGGAATAGAGATACAAAATTACAGATAGATTAGCGAAACTGTGCC ACAAAACCTCTTCAAAATTAGAAGCATGATTGTCTACAACTCCACTTCAAAAAGGAG CTGAACCAGTCCTTCGAAGGGTGTGCTTTGGTTGTGGTGGAGGTACAGAAGGCAG CAATTTCTCCAAGAACTGCTGTTTTTTTAGCCTCTCATTCTCCTCTTTAAGCTGCATC ACTTCATTCTCTAGCTCATTTGTGTATGCCTGCTTTCTTGCCCTGGATCGCACC
SEQ ID NO:78	Middle	LPS-095	GGTGCGATCCGAGTGATGGCACAAAGAAAAGCAATGATAGAAAACAAAGAACAGGT AGCTCAGAAGGTTCAGCAACTTAGAGAGTCAACTTCGAGTTAAGGAGGGCGGGAG CAATTGGCAGATTCTTCCAAATTTGTCAAGATCTCTTGGCATGAGATGACCTTATAG GATGTTAAGGAGCAAGAGGATTCTAGGAATAATGCCAAGGATAATAAGACTAAAAG GATGCTTCAAGACCAGGTGGCAAGGAAGGCTTCTAATTCAAAGGGAGTTAGCAAC GGCAACAGATGCAATTCTAGGATCGGACC
SEQ ID NO:79	Middle	LPS-096	GGTGCGATCCTAGAATTGCATCTGTTGCCGTTGCTACTCCCTTTGAATTAGAAGCC TTCCTTGCCACCTGGTCTTGAAGCATCCTTTTAGTCTTATTATCCTTGGCATTATTC CTAGAATCCTCTTGCTCCTTAACATCCTATAAGGTCATCTCATGCCAAGAGATCTTG ACAAATTTGGAAGAATCTGCCAATTGCTCCCGCCCTCCTTAACTCGAAGTTGACTCT CTAAGTTGCTGAACCTTCTGAGCTACCTGTTCTTTGTTTTCTATCATTGCTTTTCTTT GTGGCATCACTCGGATCGCACC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:80	Middle	LPZ-001	ATCTAGATCATCGATCTTGTCCAAATTTTAACTAGTGAATAGTTTTAAAAAAAAGCAA CTAGCAGAAGAGAACCTAACCACTGACAAATTGCAAATACTCTAGAACACTATTCAT CATTTTTTGCGATTCACGCTGGACCCACAAGAACCCCTTGAGCTGAACTTTCTTTTC GTTCTCCCTCCTTTTGGATCGCACCATCTAGACCATCGATCTTGTCCAAATTTTAAC TAGTGAATAGTTTTAAAAAAAAGCAACTAGCAGAAGAGAACTAACCACTGACAAATT GCAAATACTCTAGAACACTATTCATCATTTTTTGCGATTCACGCTGGACCACAAGAA CTCTTGAGCTGAATTTCTTTTCGTCTCCTCCTTTTGGATTGGACATCNAATCCTGCA GCCGGGGATTCATATTCTTAACGGCGCNCGCGNGGACTCCATNCCCCATATGATC TTTTCATCCTGGCGCNTTTAACTCTGAAGGGAAACCGGNTTNCCCTTATCCCTGGA NATCCCTTCC
SEQ ID NO:81	Middle	LPZ-002	GTGGAGTGTAAAGGTCAACGTGCCATCCGGGTACAAACTATTGTAGAAAAAATGGC AAAGTTAGGTCTGAAAATATCCATTTGGCCTGCTCTAGTTGTACAGTACATGATTTT GCACTCGCACAACAATGGACTATAATTATTTTCCTGGCAAAAAAAAAAAA
SEQ ID NO:82	Late	LPZ-003	GGTGCGATCCAGGACATGAGGCCGAGTTTGCCATTGTGATATGATTGAGGAAGTC CAGTCCTAAAATTAGGTTTATCTTGATGTTTGACAAGAGATATAGAGGGGCATGATG ATTCATTGATCTGTTTGCAGATCTGTAACTGCAACCATTCTAATGACATAATAGCGC TATTGTTTGGGTTCGTGTGATGACATAATAAATTGATTTAATTTAATAACATCTGTTA ATGCAATGGCTGTAGCTGCATCATCACCGTATCCATCGAATGTTCCATTTTTCCAAA TGTTTGTTTCCAAAACCAGAACACCAAAATGTCCCCTGCGTTTGTNTTGAAAAATAT TGGGCCCNTACTATACTATAATNTTTNGGCATACTATACTATAATGTTTCTCCCATTC CCCCCAAATGANTCCTATACAATCCTGGCCGNCTTTACACTCCTGACNGGAAACCC GGCTTNCCACTAATCCCTGGNCNANCCCTTC
SEQ ID NO:83	Late	LPZ-004	GGTGCGATCCGACTGTGATATGTGACTGGTGAACGAGAGATCCTTCTTATGAATTA ATCTGGTATCTTTATGCGAAAGCTTTTAGGGTTGCTACATGCTCTCCTCTTTTGTAT GAATTTCCATTCTAATATCAGTCTCTGTGAT
SEQ ID NO:84	M,L	LPZ-005	GGGGAGTGTCAAGGGATAAGTGGTAAGCCAGGTTTCCAGTCAGAAGTGTAAAGGC GGCCAGTGATGTAATAGATTCATATAGGGGAATGGAGTCACCGGGGTGCGCCGTT TTAGAATAGTGGATCCCCGGCTGCAGGATTTGATGGTGCGATCCTGCCCCTGATAA TTTGGTTGCAATGGAAAATGCAGTATTAGGTGCGAGATGTAAAGCCCGCCCGGAG CGGTGCATGAAGTACTGCAATATTTGTTGTAGTAAATGTGCTGGTTGTGTTCCCAG CGGTCACTATGGCAACAAGGACGAGTGCCCCTGCTACAGAGATATGAAGTCCGCA GCCGGCAAGCCCAAGTGTCCCTGATCTTAGCACTTCAGTCCAGTCGCTCACTTCTT TTATTCTTTTTTTTTATAAAAGTGACGAGGCCGTTTTTCTTGTACTTGGTGGCCATAT GTAGAGCGGTGGCTACTTCTCCTGTGTTAGGAAATGTTGCAGTACTAATAATAAGA ACTTCTTTGGCAAAAAAAAAAAA
SEQ ID NO:85	M,L	LPZ-006	GGGTTTCCTTAAGAGTTAAAGGCGCATGATGTATAGAATCATATAGGGGATGGATT CCCCCCGGGGGGCCTTTCAGAATAGGGATTCCCGGCTGCAGGATTGATAGTGCGA TCCAAGACACAGTGGAGTACCACAATGGGGATCTGGCCAGTGCTTTGTGGCTATTC ACTGCAGCTGTATTAAAACAGGAAGCCGCAAATGGCCAGAAGGCCATTGAACTTGC TGAGAGCAGACTATCTAAGGATGGCTGGCCTGAATATTATGATGGGAAGCTTGGAC GATATATTGGAAAGCAGTCTCGAAAGTGGCAAACCTGGTCAGTTGCTGGATATCTT GTAGCCAAGATGATGCTTGAAGATCCATCCCATTTAGGTATGATAGCATTGGAAGA GGACAAAAAGATGAAGCCGTCCCTCACTCGATCAGCTTCTTGGATAATGTAAAATG GGGAAATCCTAAACTTTCAGGCCACTCTTGAATGTTTTGTCACTTCTGTATGACAAA TGAGGCAATTCATAGTACATGTTGTGCAAAAAAAAAAAA
SEQ ID NO:86	M,L	LPZ-007	GGTGCGATCCCAGAGAATATTAGTTCATGTGTTGCTCTCATTTTCTTCAATATGCAG GGCAACCATTTGAATGAAATTATTCCTTTCGAATTTCAAAAACTTAATAGGCTAACTT ATCTATCTGGAGCCGATTTTCATTGACGAGTAACCTGTAAGCTGGCCAGCAAAAGC CAACAGATGTTCAGCTCGTTGGAACCAGTTGAAGATTGTAATAGAGATGGTGAATA ATCGCGGACGGCTCGGCCAATGGAATATTTGTTGCATCATCATCAAGGGGGTATGA ATTCCAAAGAACTTGTTGATTGAAATTCCCAAGCAAAATTCTGTGAAATGAAAAATTT ATTGAGACCATTGGGCAAAAAAAAAAAAA
SEQ ID NO:87	Late	LPZ-008	GGTGCGATCCAAAGAACACAAGATGGAGTTACCACAATGGAGGATGTTGGCCAGT GCTTTTGTGGCTATTCACTGCAGCCTGTATTAAAACAGGAAGGCCGCAAATGGCCA GAAGGGCCATTGAACTTGCTGAGAGCAGACTATCTAAGGATGGCTGGCCTGAATAT TATGATGGGAAGCTTGGACGATATATTGGAAAGCAGTCTCGAAAGTGGCAAACCTG GTCAGTTGCTGGAT
SEQ ID NO:88	Late	LPZ-009	GGTGCGATCTGTGTGGCTCTGAAACATCCCGGCTCCCCTCTGCACTATAATAATCC CAAAATTAAGTGAACCCAACAGAATTTGCTCATATCTCTACAGTTATTGCAGACTGA GCAAAACCCTCAAACTCATGTGACCTCTCAATAGGAGCCCACGCCCAAGATTTGTC CAGCATGTAACACACCTGATCGCCGCCACTGCAAGCACAACCGCTCACAAATATCT TGTCACACCACACTGTTGCGCAAGTTAACAATATTCATGTCTCCAGGAAAGAAATGC CACACTTCCCAACATTCTCTTTACTATTATAGAACTTCCTTGTTGCTATGGAAAAAAT ACATTCCCAACGCAGAACCCCAACGGGGGTTCCCAATANCCCATTTCCCCCCTNTC CAAANCCNNTNTGAATGCNCCCCATNCCCTATTGNATNNTTTAAATCCNGGCGCNTT ANCTGGAAGGNAACCCGNTTGCCN
SEQ ID NO:89	M,L	LPZ-010	GTTTTCCCAGTCAGGACGTGTAAAACGACGGCCAGGGATTGTAATACGATTCACTA TAGGCGAATTGGAGGTCGATCCGTATAGGTAGTTGGATGATGAACGGGCAAAGAA GGCAAAGGAGTACAGTGATGGATCCTGTAATTCCTGTTTCAGAAAACAGAAAATCT GCAATATAAGGATGGCTAAGCTTTTCAGCTATGAAAATATATGGTGCAGTGGCACT CATATCAGTTGCAGAGTTGTCAATATAACTTTTGTGAATAGGAAAGTTGTCCTCTTT TAGAGTGCAGAATCCTGCAATATAAGGATGGCTAAGTTTTTCAGCTATATGAAAAT ATATGGTGCAGTGGCAAAAAAAAAAAA

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:90	All	LPZ-011	GGTGCGATCCTACAGAGAGCAGCTTGACGAGGGCCAAGGTTAAGGATGAAGAA TGACCTCAGCTAGTAAGGTTTACAGAAGCAGCAGAGGCATCTTAACTGTTTTTATGT TTTGGCAAAAGTTGTTGCGTCGGTTGTTTAATCCAGGATTTCAGATGTATTTTGTAG A
SEQ ID NO:91	Late	LPZ-012	ATTGTAATACGACTCACTATAGGGCGAATTGGAGGGTCCGATCCTGCGAGACCGA GGGTTCATTTTCCTTTAGACAACGACGTTCAGTGGCGACCAGAGTTTCCCAATCAC TTCAGCGATTCTATTCCTTCGTTGTAATAAAGCTTAAGGAATGCATGCTTTATTCCTT GGAAGGTTTGAATATTTATATTTATTGGCAAAAAAAAAAAA
SEQ ID NO:92	Late	LPZ-013	AGGTGACCGTCAAAATGATTGCAGAGGACTTAGAGAGGGAAAACCGTTCCGATCT GGTGAAGCAATTGGATGAAGCAGCTCTGGAATTGATTCCCGTTTCTGATGATATCG TACGGCTAAGCTCAGCTCTTCAGGCAATTGGCAGAGAATACGATTCTTCAAATGAG ATGACAGATTTTAAGAAACTTATAGATGAACATATTTCCAAGCTTGAAGCGGATTCC CCTACGGTCACCT
SEQ ID NO:93	Late	LPZ-015	AGGTGACCGTAAAATACTATGAGAAATGCTTTCATCAGGCACCGCTGGTAGGTTTT CTTCAAGCTTTTCATTAGGCAAAAGAGGCTCCGTGAGTTGATCGTTAATTCTCTCCT TGAATGGCCATATTGACCAGACACTCTGATTAGAAACTGGAATACAACTGCACATAT AGTCATTCTTATATGATTCATCCTTCTGCACTTCAGCATCCTGCGGCAACTCTTCAT CCCGCCATACTGCAGAAAAATTATTTGACTCTTGATCATGTTGTAGATGAATCTTCA TGAATCTTCTCATCTTGCATTCTTGTCTTTATATCTTTAGGAAATTGCATCTGGTAAA AGTATAAATGCATCTTCACTGGTTGCTTCAGTTTTTGCATGCTCCTGTTCTTCTTGTT TACATGTGATCTACCAAATCATCTAATGTATTCTCTCAATGTCTTGTGGACATTCTCC TTCATTCCGAGATTACCAATCATCTACCCGAATAAATGTTGCCCCGTCAGCAATGCC GTTTTGGTCC
SEQ ID NO:94	Late	LPZ-016	AGGTGACCGTAGTAGGCGTCCAGAGGCTGACAAAATCCCAGGCCTGTGCAAATCT GGAAGCCGCATGCAGGGCCGTGGCACCTTACACTTGCGGCCTTAACAAAGTGGCC CGCGGGACCCACTTCTACCAGTGTGTTTATATTCTTGTGCAGCCAACACCAGAGGT TATGCAGGCGAATGTGCTGGCCAAGCGTTGTTTCGGCTTGTCCGCAAACCCTCTC GAGTCTTACATGCCGCATATGAGTCTTGTGTATGGCGATTTGCCTGACGACGAGAA AGAGAAGGCCAAGGTTAAGGCGCAGCTAAATTCGATGAACTTATCCGCAACACGGA ATTCCAAGTCTCCAGCTTGTGCTTGTACTCGACAGATCTGAAAATAATCCTCACTCA TGCATAAGTGCAAAATGTGATCTTAACCTGCTCTGAAAATTACATAA
SEQ ID NO:95	Late	LPZ-017	AGGTGACCGTCCACGAGAATTTGGCTTCAAAACCGTAGGAGAGGGATATGAACTTG CCAAGGCACAACTGACGCATGAACAAGACGTAAAATGACTCATTAGACACTGACAT GATAATGAAAAACCTATGAATGATGATAGACTCAGCTACTTGATGACATCGCCCGC CATTTGGACATCTTTATAAGGAGTTTAAGCAAACCCTAGACCTACTGCCTAGTGACC AACTTTTGCTTGACGACTCACTGAAATGACAATATTTGACCTTGACACTTCAAAATC ACTTTGTAGGAACTCATTTGATCACTGGAGGACGGCTGGAAAGACTGACACTAACA GGACTTTATATATGCACCTCGTCTATCCGAACTT
SEQ ID NO:96	Late	LPZ-018	AGGTGACCGTAAGCACAAGTCGTCAAAATTATCTCTATTCCGGCAGTAAAAACCTAT AGCTAATGATGGATCAATAGCACTAAGTGGCAGCTGGCGTACATCACTGCAATGAT AAGAACCAGTATCAACCCCCATATTATCAGGAGATATCTCCACCACCTGCTGCACT ACATGTGGATCTAAGTACAGAGCCTGATCATCCTGAACACCAACAATATACGTTGAA GCTCCAGGCTTTCCACCAGCAATACCAAGACTTTGGGGAAATGTGAACGTTTCACG AAGTGATGGTACATACCTTGGGTTGATCTTCTCTACACCAAGAACAAGCGGCACCA AAATCAGGATAGGCACTTGGTCTTCCCCTTCTCCATTGGACCAGTCTGAACACAGC CTCGCAGCATCATCAATGCAGATAACTGGAGTCCCTCCACGGTCACCT
SEQ ID NO:97	Middle	LPZ-019	AGGTGACCGTGAATATGGTGGGTATTTGCAGGGCAAGATTCAGGATGCTGCTCCC GGAGCTTAAGTAAGGTCTTGGACCCTAATAAATTCAGGGTATATGCATTATGTATAT GCTCTCATTTAGCTGCTCATCTGATTTCCATTGGGTGAATCAGTTGTTTTGCAGTAC GTGGGGGTCTGTTTATTTTGTGAGTTTATGGTGGAGTTCATTTTGTTGTTGTTTT TTTCTTATCTAGGGTTTAGGGTTTTGCCCTGTAATCGGTCTTCCCCTCTCTCCTGCG CTTGAATTTGACCTGAAACCTCTTGAAGTAGGCCCTGGTTTTCTGGGCTTTGACGA AAACCATGGTTGTGGATCTCCTCTCTCCTGCTACGGTCACCT
SEQ ID NO:98	Late	LPZ-020	AGGTGACCGTCCTACTTCACCGCAGTGACTTCCATCTGGTTTTAGGAAACTATCCC TAAATCCTTCACTAGTTGACGAATTGATTGACTCAAATCAACTGTCGGTCAAACCCA CTCTCTCTGAAAGTGAATTCTATGAGTCTATACCCAACCCAAATCAATAGGTTGAGG TAACAGTTGACCCGATTTCACCTTCAACAAATCATACCTTTCCCGAAGAGAGTGAAC ATGATTCAACACAAGTTCTTTTTGGTTCACCAGATTCAAATGAGCTTGGGGGTAATC CTCCTGTTCCATCAAGACAAGAAGAATCCTCCCACTCTCGTAACTCAAGGGTTAA TCCTCCCATTTCTACGGTCACCT
SEQ ID NO:99	Late	LPZ-022	AGGTGACCGTCNCGGGATAGNTGGAGCCNAACAAAGTACNGAANAAANTGAANCG CNCTGGGAAGCGNGCNGAAANNTGGNCANACNTGCCCTNCNACTCGGTTACCCAG CCNTTCTCTACCNANAATTATNACNNNANAGCNCCATGCTGGGTTTGTNANAAAAN AACNGCTNTTGATAAAATTACATAGANTNNNGAACACGTTAAGAGGAATATGGTTCC ANATNCATTNTNAATNANNANTTAAAAACTNNNTATGTNCTAGNGTCNCCT
SEQ ID NO:100	Late	LPZ-023	AGGTGACCGTACAGCACAGGTATACAAATCATAGAAATGGGCTTCTGTCCAACTGT CAGCAGAAGCGATATGAAACCCAGAAGCATCAACTCTGCTTTCAATTTTTCAAGCG CTTCATATAGAGCCTTTTTATTTCTTCTGGAGAGCCAATTGCTAGCATAATGAATAC CATGTTCAAGAAGTAAAGAGATGACCACAAATGCCAAACAAACAACTGCTACTGCC CAAGTTAGGAGTTTGCTCTAGAGAACGGTCATTGCCACGGTCACCT
SEQ ID NO:101	M,L	LPZ-024	AGGTGACCGTGGATATGGGAGCAGAGCCGTCCGCAGTGGATGCTGCAATTCAACT TGAAGTGGCAGAAGCTGTGAAGACTCTCCAAATGGACAAGGCACGAAGACAAAAC CAAGACAAGGATGAGGGCAAGAGTGGCAACGCTGATTCAGATGACTTGAATGAAAT GGAAGTCAAAGCTAAAGCAGCCGAACAACTGCTTGCTGTGCATGGGGCAGCATTA CTACAGAATGCTCTGAAAGAAAATTTGTCGAGTCATGAAATGCGGGTTGGTTCAAA TACAAGGGAGGAAGGTGAAGTTAGAAAGAACAGAAAGGGCATCAACGCAGACCCC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			TCACTGATATCGGCAACACTACGGTCACCTAAGCCAATTCTGCAAATTTCCATCACT
			GGCGGGGCCCGCTCCAACTTCCTCTAAAAGGCCAATTCCCCTATATGATTCTTATT
			ACAATCCCTGGCCCTCCTTTTCCACTTCT
SEQ ID NO:102	M,L	LPZ-025	AGGTGACCGTAGCAGGAGAGAGGAGATCCACAACCATGGTTTTCGTCAAAGCCCA
			GAAAACCAGGGCCTACTTCAAGAGGTTTCAGGTCAAATTCAAGCGCAGGAGAGAG
			GGGAAGACCGATTACAGGGCAAGGATCCGCCTGATTAACCAAGATAAGAACAAGTA
			CAACACACCCTTGCCAAAAAAAAAAAAAAAA
SEQ ID NO:103	Middle	LPZ-026	AGGTGACCGTATGAGCAAGGAGGGAACAGTATGACAGGCAGTCAAAGCCCACGAG
			GGGTGCCCCACTGCCTGCAGCAGCGCACTTACTTGGACTAACAAACTTGTATCGTG
			ATTAAAACGATGAACATCGTATTGTGGAGTGGAGCCACTCGTGACCTGATTCTGTC
			CTAAGTACTTGGTCCTGGAATACAATATTGCACGGTCACCT
SEQ ID NO:104	All	LPZ-028	AGGTGACGGTCAAAGTACAATGGAGTCATATATCCACTTGAATTGAAACCTCTAATT
			TAAAAGTTCTCAAAAAATATTTTATTTACAAAACAGGGAAAATAAAAAATGACTCTAT
			CAACTATACAATCCTAACATCCATCTCCCGACAGACCTCCAGTATATGTACAAGGC
			GCTGAAAGAAGGCTGATTATTTTCTATTCCAGCTCGCATAACGTGGTTCTTCTGAG
			GCTTTGCCTATTCCTTTCTTTAAAATCTTTCGCACGAAAGATTGGCATTGACCTTCG
			GCTAAATCTCAGACTCCAGGGAACCTTGGACTCCCTTTAAAACCTAGAGCTACTTTT
			TACGAACGCCTGCTTCTCTTGAACACTTAGGGAACTTATACTTACAAAACTTCGGGA
			ACTCCACCCCCTAGCTTTGCAGGACTCCAGCAGATTCCCCAAACTGCCAGAAGGCA
			TATTTCCATGCACTGTTAGGGGTGAATTCCTACTATCAAAACCCCCAAAACATCATA
SEQ ID NO:105	Late	LPZ-029	AGGTGACCGTATGGGAACAAGTATGGGAACAAGAACGTTATTACATAAAAGATGGA
			GATGCAACACAGCATAAATTGATGCTAAGTTTGTTACAATGATGCATACAGCTTAAC
			CAAGCTTGGAAATGACATCATTAAGTGCGGTCACAGCCTCTGCATAGTATTTCTCT
			GCCTTGGGTGTATCCTTGCTCCTTGCAGCGTAGTCCAGGTTGTCAAGGGTTGTCAA
			AAAGCTTGGTGGTGAAGGTTTTGAGGGGCTTCTTCTGGTCCTTGGGCTTTGAGGA
			GATAACGGTGTTTGAAGTCCTTAGCGAAAGTAAGAAACCTTTGGAACCGAAGTCCG
			TTCTTGACGTTACCGCACGCCTTCCTTATCTATCACTTTTTCACCTCCAGAAATTGC
			TTCCCGAATCCCTTGCTCTCCCACCCCCTGTTCCCCC
SEQ ID NO:106	Late	LPZ-030	AGGTGACCGTAGTGTTGCCGATATCAGTGAGGGGTCTGCGTTGATGCCCTTTCTG
			TTCTTCTACTTCACCCTCCTCTCTTGTATTTGAACCAACCCGCATTTCATGACTCGA
			CAAATTTTCTTTCAGAGCATTCTGTAGTAATGCTGCCCCATGCACAGCAAGCAGTTG
			TTCGGCTGCTTTAGCTTTGACTTCCATTTCATTCAAGTCATCTGAATCAGCGTTGCC
			ACTCTTGCCCTCATCCTTGTCTTGGTTTTGTCTTCCGTGCCTTGTCCATTTGGAGAG
			TCTTCACAGCTTCTGCCACTTCAATTTGAATTGCAGCATCCACTTGCGGAACGGTCT
			GCTCCCCATATCACGGCACCTT
SEQ ID NO:107	Late	LPZ-031	AGGTGACCGTAGTGTTGCCGATATCAGTGAGGGGTCTGCGTTGATGCCCTTTCTG
			TTCTTCTACTTCACCCTCCTCTCTTGTATTTGAACCAACCCGCATTTCATGACTCGA
			CAAATTTTCTTTCAGAGCATTCTGTAGTAATGCTGCCCCATGCACAGCAAGCAGTTG
			TTCGGCTGGTTTAGCTTTGACTTCCATTTCATTCAAGTCATCTGAATCAGTGTTGCC
			ACTCTTGCCCTCATCCTTGTCTTGGTTTTGTCTTCGTGCCTTGTCCATTTGGAGAGT
			CTTCACAGCTTCTGCCACTTCAATTTGAATTGCAGCATCCACTGCGGACGGCTCTG
			CTCCCATATCCACGGTCACCT
SEQ ID NO:108	Late	LPZ-032	AGGTGACCGTCGTGAAATAGCGAGAACGGCGTGGAACATCGCAACGGCGGGGAG
			GCTGGCGGACGTTGCACGTTTCTGGAAGGTATGCGGCTCTCTCCTCCGCCTCAGT
			TTCCATGAAGAGGTCCTCCCTGGTTGAATCATACGATTGCGATTGATCGAGTACTT
			GCTGTATGGCTCGGCATCGGCATTGTGGAGACATTCTTTCCTATTCCTCGCAGCAT
			CTCTCCGATGGTTGCTCTCTCCGGAGCTCCATGTTATCCCCGGCACTGAGACAGTC
			GCTGCCGAATCGCAAGAGCTTCTTTGTTTTTTGCAGGCTTCTCCAAACATAATGCCT
			CCGGGCCCCTCAACCGAATTCTGCCAAATCCACCCC
SEQ ID NO:109	E,L	LPZ-033	AGGTGACCGTGGACGACAGTGAGTGCAGTCATCATGCTCTCCAGTGGACTTTAAG
			CAATCTGCATCTTTATGGAAGTGATGTATCTCTTGTGGTTTTTCATGCTCAACCATT
			GGCAGTCTTCAACAGTGCTGCAACAATGGGCATAACGTCTCCCGAATTAATTGAAA
			CTATTGTGAATCAACAGATAGGTTTCTGGTCACATCTAGCAATACAAACACAAATAA
			CTGTGGAACAGAGCCACAAAACTATGCTTCAGAGCATCTAATTACACATATCTTCTC
			TAAAACCCTTGCATAAAAAATAAACTGAATCTCGACCTTAGCACTATTGCCACCATC
			ATCTCAAGCAAACATTCTCTAGAATACCATCTTCACAATGCACTAAAGTTACATAAG
			CACTGAACTTAAAACATTTCTGTGACGAATGAAGGACCAATTCATCATAGTCAGCCT
			TTGCATCCAATCTGTTGAATGTGCTGAAAAATGCCCAATAAACGTCCATCCAACACT
			GTCTTCCTCTCTGAGGTGCACACTGATTTCTGCTGCTGAACCAGTCGGGATTCCCT
			GCTCAACGTCCC
SEQ ID NO:110	Middle	LPZ-034	AGGTGCCCGTGGAACTACTGTTAAATCTGGAATCCCTTGTCTAGCTGTAAAAACTC
			GACAAGTGCATGTTGGTATTAGTAGGGTTAACAGAAGGGTTCTTACCCAGATTTAC
			CCCTTTGGCGGAGATATTTAAAAAAAAAGAATTGTCATTATGGTAAATAGGTGTGAC
			AGGTTATCAATAGAATAACTGACGAGAGTAAACTGATAATTATTAAGGTTAAAGTGT
			TCGTAAAGGAGACTTGGACTCTAGGTTGGATGCCTACACTTAGAGCCGTTCCCGCA
			CTTGGACGGTCACCT
SEQ ID NO:111	Middle	LPZ-035	AGGTGACCGTCCAGTGCGGGAACGGCTCTAAGTGTAGGCATGCACCTAGAGTCCA
			AGTCTCCTTTACGAACACTTTAACCTTAATAATTATCAGTTTACTCTCGTCAGTTATT
			CTATTGATAACCTGTCACACCTATTTACCATAATGACAATTCTTTTTTTTTAAATATCT
			CCGCCAAAGGGGTAAATCTGGGTAAGAACCCTTCTGTTAACCCTACTAATACCAAC
			ATGCACTTGTCGAGTTTTTACAGCTAGACAAGGGATTCCAGATTTAACAGTAGTTCC
			ACGGTCACCT
SEQ ID NO:112	Late	LPZ-037	AGGTGACCGTATGGGAACAAGAACGTTATTACATAAAAGATGGAGATGCAACACAG
			CATAAATTGATGCTAAGTTTGTTACAATGATGCATACAGCTTAACCAAGCTTGGAAA
			TGACATCATTAAGTGCGGTCACAGCCTCTGCATAGTATTTCTCTGCCTTGGGTGTA
			TCCTTGCTCCTTGCAGCGTAGTCCAAGTTGTCAAGGGTGTCAAAAAACTTGGTGGT

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			GAAGGTTTTGAAGGGCTTCTTCTGGTCCTTGGGCTTTGAAGAAATAACGGTGTTGA
			AGTCCTTACCAAAGGTTAATAAACCTTTGGAGCCGAAGTCGTTCTGGACGTACGGC
			CACCCCTTCCTTATCTATCAGCTTTTTCACCTCCAAGAATTTGCTTCCCCGAATTCC
			TTTGCTCTCCCAGCCGCCTGGTCCCCCGAAAAGGGCTGAATATAAAACCGTCCTCA
			ACGGCATTCCATTCCTCCCTCGTCTGAAACACTTCCCCGGTGCCCCCGAGGTGAA
			GGGCCATCAACTTGATGAACGGCTTTTGCAAGGCTCTGACCCCGGCCCCGTCACT
			AACCAATTCTGCAATC
SEQ ID NO:113	Middle	LPZ-038	AGGTGACCGTGGGGAACAACTACATGACAAATCATTTCTTTGTGGTGGATGTACTG
			GACACCAAATAAGTGTTGAGAGTCCACTGGCTCTGTACGCGTGGCAGAATCACAAC
			GGACTTGAGAAAGTTGAAGATGGAATTTGTATCGCTAGATGGCCAGACCATGTTGC
			TTCAAGGGATGCACTCGTAACCCCCACAGTCTGTCTCTACCCACTAGATGGAGGCT
			GACATGAGACATGGAGACATTAATTGGGTTGTGGAGTTAAAGATCTCTCACGTTCG
			GGGAAAATCCAAGCCATCATACTTATATATCCGTCCCGTGCATGTAACCTCCTCCA
			CTCTGTCCCTTAGGCCCGTTGTTGCCT
SEQ ID NO:114	E,L	LPZ-039	AGGTGACCGTATGAGCAAGGAAANNACCGCACTGGCTCCCAGCAGCATGAACANC
			CAGGTCCCAACCATANACCNCNTGGAGAANGTGATCAAGATATTAGCGACAGTGTN
			ATTGTACNTCTCNCCAAACACATTATACACGATAAGAGAGCNTAAACTACTCTATTC
			CTTTGACGNAGTGACTACNTGAGTANAAGCGATCATTATCTTGCNAACTTTGCATGA
			AAAACAACAAACCCACNTCCAGTTTCTCTATANTCTGGCCCCACNATGAATAANANT
			CCTGCCATAATAATGANTCTTTGTCCCCANACANAAATTNNATAAGACAGGAGCCC
			ACTGTTGCTTGCATGACTACCANTCACTTTAAGGCGTTGCGAATCCCGGTCCTAAC
			CATCTGCATACCATNGGCANNCTTTACTTTCCAACTGCCCAAGACTGTGAACAGGG
			CGGTTCNNACCCTATAANTTTTAGCCTCTNNTCGAANCNCTTNTTTTCGTTCCCCGG
			AAANCCGNTTCCCACCCTTTGGAACCTTTTTTTTTTGCCGGGCCCCAGGCNAATTC
			TNCAATTCCCCNCTGGGGGG
SEQ ID NO:115	Late	LPZ-040	AGGTGACCGTGGCGGAGGTTAGGGAAGTTTGACTTCTCATTTTCTCACGCACTCCT
			CTCCCTCGTAACCTCGGTCGAGTCGATGGCGGCTTTTTAGTCGAGTGTGCTAACG
			CACCCTCCGGGCCTCAAAATTTCCAGCTACTCGTATTTGATCAATGCTGAAATCGC
			GTAATCACGTAGATAATAAAGCGTAATGAATTCTATAATGAAGCATGTTTCTCTATA
			GTTCATGTTGCCGAGAAGGAATAATGAAAATGAAGCCTTATATATTATCTGGGGCTC
			AAGGAGATGTTATCTTTTCTCTTCCTTGGTTAGAGACCGTCACCTTCACTTTGAATT
			GGATAAAGCTTCATTTGTTTAAGACCTCCCACCCGTAAATACATACGGTAGCCTTCT
			TATGTTAGAAACATACGTCACCTACGCAGAATTGTTAGAATGAAATGA
SEQ ID NO:116	Late	LPZ-041	AGGTGACCGTGGAACAAGATGATTAGTTCTCATGCGGGCCAGGATGATTAGTTCTC
			CTATGGCAACTGTTGGACAGGATGATTCGTTCTCCTGTGGACAGGATGATTAGTTC
			TCCTATCGAGGCATCCTACCCAAGCAGTTTGGGACTCATGGGAAGTACCTCTCATC
			TGATCAATGAGTAGGAAATGGGGTTAGGGACCATTAAGTAGTATTATCGATGGATG
			CATTGTTGTATCTATTGTACTCCCTATGCTAGAATGAACTCCATTGATCTGGGATCA
			ATGAATACTGTTTCTGGGAATCATTGAAAATTTGTATGAACACACTCTGAACACTGA
			ATTTCCGGTTCATTGGAAGAGATGGTTTTAAACACTCTCCTCATCTCATTTCTTCCC
			CTTCCTTATTCCAACCAAATTTGGGCCACCCTGCCAGGAAATTCATTTGATGGTTGG
			AAAATACCACGGGCCCTAACCAATTCTGCAA
SEQ ID NO:117	Late	LPZ-042	AGGTGACCGTNCATCTCTACCATNATNCCTCCCTCCCGNCTGTATCANCNGGCNTN
			NANGTCNTTNNCTANNNNAAGNTTAATCCTATCCCNTTANAGTTGACGGTCTCTAN
			NCCTAGAAGAGAANCCATAACATCTCCTTGAGCNACACATGGGATATACCGCCANC
			TTATNTAATACTTTCNCNGCACGGTAACNGACCANAANCATTCTTCACTATAGAATT
			CATGTCGCTTCATTATCTACCTCATTNCNCCANATCCCCCTTNATCTCATNNATTTAT
			CTAGAAANTTCTGAAGNTCCNNAAGGGTTCGTTTTGCACCNCCCCAANTAAAAAAN
			CCCTNCCGNTTACNTCGAACGAAGGTTTTCAAANGAACAGNAATTCCTTTACAAAAA
			TCAANAATTTTAACTTCCCNAATCCGGCCCCCCNGTNCCCGAAACCCNATTTCTAC
			GATTGCATCACCCCGGGGGNCCNCTCAANCCNNCTTCTTAAAGGNCCATNCCCNT
			NNNTGATCCTCTNGCATCCAANGGCNCCTTTCCACTTTTATTGGAAAACCCCCNTT
			CCCCNTTTTACCCTTNNAAGGCCCCTTCCC
SEQ ID NO:118	Late	LPZ-043	AGGTGACCGTGGAACTACTGTTAAATCTGGAATCCCTTGTCTAGCTGTAAAAACTC
			GACAAGTGCATGTTGGTATTAGTAGGGTTAACAGAAGGGTTCTTACCCAGATTTAC
			CCCTTTGGCGGAGATATTTAAAAAAAAAGAATTGTCATTATGGTAAATAGGTGTGAC
			AGGTTATCAATAGAATAACTGACGAGAGTAAACTGATAATTATTAAGGTTAAAGTGT
			TCGTAAAGGANACTTGGACTCTAGGTTGGATGCCTACACTTAGAGCCCGTTCCCGC
			ACTTGGACGGTCACCT
SEQ ID NO:119	Late	LPZ-045	AGGTGACCGTGGGGGATGGGGCCGTGGGGAAGACTTGTATGCTCATCTCCTACAC
			AAGCAACACGTTTCCAACGGATTACGTGCCGACTGTTTTTGACAATTTTAGTGCAAA
			TGTGGTTGTTGATGGCAATACAGTAAACCTTGGCTTGTGGGACACTGCAGGGCAA
			GAAGATTACAACAGACTGAGGCCATTGAGTTATAGAGGTGCAGATGCTTTTCTGCT
			TGCCTTTTCTCTGATCAGCAAGGCTAGTTATGAAAATATATCAAAGAAGTGGATTCC
			AGAACTTAGACATTATGCACCAAATGTGCCAATCATTCTTGTGGGAACTAAATTAGA
			TTTGCGTGATGACAAGCAGTTCTTTGCTGATCATCCTGGAGCAGCCCCTATAACAA
			CAGCTCAAGGTGAAGAGTTGAAGAAGCAGATTGGAGCAGCAGCATATATTGAGTG
			CAGTTCCAAAACCCAGCAGAATGTCAAGGCTGTTTTTGATGCTGCAATTAAAGTGG
			TTCTTCAGCCACCAAAGCAGAAAAAGCGGAGAAAAAAGCAGAAAAATTGTTCTATTC
			TCTAAGAAAAATGTGGATGTTCTGAACGCNCTTCACTGACAATAANGNTGACGTNG
			GAATATCTTCCTCC
SEQ ID NO:120	Late	LPZ-047	AGGTGACCGTAAGCACAAGTCGTCAAAATTATCTCTATTCCGGCAGTAAAAACCTAT
			AGCTAATGATGGATCAATACCACTAAGTGGCAGCTGGCGTACATCTCTGCAATGAT
			AAGAACCAGTATCAGTCCCCATATAATCAGGAGATATCTCCAGCACCTGCTGCACT
			ACATGTGGATCTTAGTACAGAGCCTGATCATCCTGAACACCAACAATATACGTTGAA
			GCTCCGGGCTTTCCACCAGCAATACCAAGACTTTGGGGAAATGTGAACGTTTCACG

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			AAGTGATGGTACATACCTTGGGTTGATCTTCTCTACACCAAGAACAAGCGGCACCA
			AAATCAGGATAGGCACTTGGTCTTCCCCTTCTCCATTGGACCACTCTGAACACAAG
			CCTCGCAGCATCATCAATGCAGATAACTGGGCGCCCTCCACGGTCACTT
SEQ ID NO:121	Late	LPZ-049	AGGTGACCGTGCCATAGCGCATGGCGTGTAACTGGATGAGACCGCATGGCTCAAA
			TCTGCTAGGAATCAACATGAAATCAGCTCCAGCTGTTATCATATGAGCAAGTGGCA
			CGTTAAACTTTGCTACTCCCCTGACGTTGTCTGGATATTTCTCTTCAAGCTCTTCAA
			GCTGCTTCTCCAAGTACTTTTTACCGGTGCCTAGGATAATTAACTGCACGTTTTCAT
			CTGCAATTAGAGGGACAGCTTCAGCAAGAATATCTGGACCTTTCTGCTCTTCAAGT
			CTTCCAATAAATCCTATAACAGGAATATCTGGATCCACGGTCACCT
SEQ ID NO:122	Early	LPZ-051	ATGTGACCGTCAAAAGGGCATATAAATCGGGGAGCTCAATGGCAAGAATGTACGAT
			TTCTGGCCTCAAGTCGCCCTGAATTTGGTCAACAACATCTTGATAGAGCGAGAGGA
			CGCTCCCAATTAAGATCTGGAAACTGTCGAGAGTGATTGAGGTCATTTTTAATCTAA
			ACTGAATTGTGGGGACAATTTTTCAATTCAGATCCTTCTAGCAAAGCAAAGCAAAGC
			TTAACAGTATTGTATCCATGAGAATGGATTCTGCACAGGTCAGGCTCCACGGTCAC
			CT
SEQ ID NO:123	All	LPZ-053	AGGTGACCGTGGAGAAGAGAACGCTTTGCCGACTCTCTGGGATGCCCTTCCCTCC
			ATAGCCGTCGTGGGAGGACAGAGCTCCGGGAAATCCTCTGTGCTGGAGAGCATCG
			TTGGAAGGGATTTTTTACCGCGTGGATCAGGTATTGTTACTAGACGGCCGCTTGTC
			CTTCAACTTCACAAGACTGATGAAGGCAGCAGGGATTACGCCGAATTCCTTCACCA
			ACCCAGAAAGAAATACACCGACTTTGCACTGGTAAGGAAGGAAATTGCGGATGAGA
			CTGATCGAATTACAGGGCGTTCCAAGCAAGTCTCAAGTGTCCCAATTCACCTTAGT
			ATTTATTCACCCAATGTTTGTAAATTTGACTCTAATTGATCTCCCTGGGTTGACAAAA
			GTGGCTATTGACGGTCACCT
SEQ ID NO:124	Middle	LPZ-054	AGGTGACCGTGCAATATTGTATTCCAGGACCAAGTACTTAGGACAGAATCAGGTTA
			CGAGTGGCTCCACTCCACAATACGATGTTCATCGTTTTGATCACAATACAGGTTTGT
			TAGTCCAAGTAGGTGCGCTGCTGCAGACAGTGGGGCAGCCCTCGTGGGCTTGGA
			CTGCCTGTCATACTGTTCTCTCCTTGCTTCAGGCTCTACTGCTGTTGCTGCTGCTG
			ATACGGTCACCT
SEQ ID NO:125	Middle	LPZ-055	AGGTGACCGTACATACAAGGTCTTATCACCAGCAGCAAGAATAATCAGTTGGCCAT
			CTTCTGCAGGCTTCTTGCTGCCTGAGACAGGAGCCTCAAGAAATCTTCCCCCCTTT
			TCAATGATTGCCTCATTGATCTTTGTTGAAGTGATAGTATCAAGTGTTGACATGTCA
			ATGTATCCTTTTCCTGTACACATTTGCTCTAGGACACCATCCGAGAGGGCAGCAGG
			AGGATCAGACAGGATGGCTATGGTATAGTTGCACTTCTTTACAACTTCGGCAGGAG
			TGCTTCCTATGGAAGCACCTTGCTGAACAAGTTCTTCACACCTAGACATTGTCCTAT
			TCCACACGGTCACCT
SEQ ID NO:126	Late	LPZ-056	GGTGACCGTACATACAAGGTCTTATCACCAGCAGCAAGAATAATCAGTTGGCCATC
			TTCTGCAGGCTTCTGGCTGCCTGAGACAGGAGCCTCATGAAATCTTCCCCCCTTTT
			CAATGATTGCCTCATTGATCTTTGTTGAAATGATAATATCAACTGTTGACATGTCAAT
			GTATCCTTTGTCCTGTACACATTTGCTCTAGGACACCATCCGAGAGGGCAGCAGGA
			GGATCAGACAGGATGGCTATGGTATAGTCGCACTTCTTTACAACTTCGGCAGGAGT
			GCTTCCTATGGAAGCACCTTGCTGAACAAAGTTCTTCACACCTAGACATTTGTGCTA
			TTCCGCACGGTCACCT
SEQ ID NO:127	Late	LPZ-057	AGGTGACCGTGGAGGGGCTCCAGTTATCTGCATTGATGATGCTGCGAGGCTGTGT
			TCAGAGTGGTCCAATGGAGAAGGGGAAGACCAAGTGCCTATCCTGATTTTGGTGC
			CGCTTGTTCTTGGTGTAGAGAAGATCAACCCAAGGTATGTACCATCACTTCGTGAA
			ACGTTCACATTTCCCCAAAGTCTTGGTATTGCTGGTGGAAAGCCTGGAGCTTCAAC
			GTATATTGTTGGTGTTCAGGATGATCAGGCTCTGTACTTAGATCCACATGTAGTGC
			AGCAGGTGGTGGAGATATCTCCTGATAATATGGGGGTTGATACTGGTTCTTATCAT
			TGCAGTGATGTTCGCCACTGCCACTTAATGCTATTGATCCATCATTAGCTATAGGTT
			TTTACTGCCCGGAATAGAAATAATTTTGACAACTTGTGCTTACGGCACCT
SEQ ID NO:128	Late	LPZ-058	AGGTGACCGTGGAGGGGCTCCAGTTATCTGCATTGATGATGCTGCGAGGCTGTGT
			TCAGAGTGGTCCAATGGAGAAGGGGAAGACCAAGTGCCTATCCTGATTTTGGTGC
			CGCTTGTTCTTGGTGTAGAGAAGATCAACCCAAGGTATGTACCATCACTTCGTGAA
			ACGTTCACATTTCCCCAAAGTCTTGGTATTGCTGGTGGAAAGCCTGGAGCTTCAAC
			GTATATTGTTGGTGTTCAGGATGATCAGGCTCTGTACTTAGATCCACATGTAGTGC
			AGCAGGTGGTGGAGATATCTCCTGATAATATGGGGGTTGATACTGGTTCTTATCAT
			TGCAGTGATGTACCCACTGCCACTTAGTGCTATTGATCCATCATTAGCTATAGGTTT
			TACTGCCGGAATAGAAAAATTTTGACAACTTGTGCTTACGGTCCCT
SEQ ID NO:129	Late	LPZ-059	AGGTGACCGTGCTAGGACACACAATTTCTCAGCAAGGATTACAGGTGGATCCTAAC
			AAAATTGCTATAATTCAAAAGGTTCCACCTCCTTAAAAGGTAAGAGATGTTTGGAGT
			TTTCTAGGCTTGGCAGGATATTATAGAAGATTCATCAAAGATTTCATTAAGCTAGCC
			TCGCCATTGTCTAGCCTCTTAGGGAAAGATGTTGAGTTTCAATGGACTGATGACTG
			CCAAGGGGCTCTGGATGAGTTGAGAGATAAGCTGGTATCCGCCCCGATCTTGAGA
			GGTCTAAACTGGGCCCTACCTTTCCACATCCACATTGATGCCTCGAACAAAGCCAT
			AGGGGCAGCCTTAGGACAAGTTGAAGAGAAAATACCATATGCCATATACTTTGTCA
			GCAAAAATCTGTCTAAGGCAGAACTGAACTATACGGTCACT
SEQ ID NO:130	Late	LPZ-060	AGGTGACCGTCATATTCCCCTCTATAGCAGCACTAACAATCCATTTTCTGAGTGCAT
			CAGAAAATCAACAGACGGTAAATGTCTTGAGACTAACGAGAAATTAATAATCACGTT
			GTACAAAGAACAGTATGTCCCGTCACGTCACGAGTGCCCTGAGAGATCATCCAACT
			TTCTCTGAACCCTCGTGTTACACGCACGCAAAATCAAGGATCAGTTGTAGTTATTGC
			TGGCGTGACAGACGTGACACCTACTGTTCCGCTACAAACGATATAATTGAATCCAT
			GATCGGATTATGTATTATGATCTTAGCGCAGTGGTTATGAAATTATGATGAATTTGC
			TTATGATTTTCTCAGCGTTTGTGGAAGAATCTCGCTATTGAAAACTTCCCCGTATAT
			TTCCAAACTTATTATCATCCCACGGTCCCT
SEQ ID NO:131	Late	LPZ-061	AGGTGACCGTACAGCATTTATTGATGTTCTATTTTGTTGTTTGCAAGTTTTTCCGATT
			CGCTGTGAGGCACGGAAAACGAGATAAGTTGTAAAAGTTTGCTCGCTGATTTGAGG

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			CACGGAAAACGAGATAAGTTGTAAAATTTTGCTCGCTGATTTTTTGCTGAATATTTC
			TCTCACTATAAAAAGCATTTTCCAGAAATAAGAAGGAGCTTTCGAACTGGTTTTCCC
			CAAGAGTTGTAGGGGGTTTTTCCACGGTCACCT
SEQ ID NO:132	Late	LPZ-062	AGGTGACCGTATTTATGGTCGCAGGCACAAATTCTGCTACTGTAGAAGGGTTCTTA
			CCAACTTTAGGTAGAAGGCGAGGAGGGCTTTATTAGTACAGTTCTGTGTAATCTTA
			ATGATATTTTTTGCACTATTATTTTATGGTAAAAGGATTGATTTGTCTTTTGCAAAGG
			CCTTAGGATTGTTTATTTACCTTTGGGCTAAGGGAGGAGGTAAATTTTTCACATTGG
			GAAAAAAAATGGCTCGGTCGTTGTCACGGTCACCT
SEQ ID NO:133	Late	LPZ-063	AGGTGACCGTGCCAGTATGACAGATGGAACCATGCAGCTAGCCACCAAATTGTAAA
			CATCAAATTTTGTCTTCAATATAAGTTGCAAATTCTTAATTAATTATGATCACCATTTC
			AACGGTCACCT
SEQ ID NO:134	Middle	LPZ-065	AGGTGACCGTGAATAGAAGCGAACACATCCTTGTTGCTGAATCTAACGACCAATCG
			GTATTTGGGTGTGTTGTACTTGTTCTTATCTTGGTTAATCAGGCGGATCCTTGCCCT
			GTAATCGGTCTTCCCCTCTCTCCTGCGCTTGAATTTGACCTGAAACCTCTTGAAGTA
			GGCCCTGGTTTTCTGGGCTTTGACGAAAACCATGGTTGTGGATCTCCTCTCTCCTG
			CTACGGTCACCT
SEQ ID NO:135	Middle	LPZ-066	AGGTGACCGTGGTAGAGGAGGCAGGCACTCATCTAACAGTCGAAAGCCCTTTACA
			AAGGGGAATGGTACCAGCATAGAGAAGAAACACAGACGGTTTGAAGAGGATGATG
			TTCCATGCATCCCACTTGGCTCTGTCCCTCAAGTTGAATATACCTGGACGAGAGGT
			ATTGCATTTCCCAACGGTCACCT
SEQ ID NO:136	Middle	LPZ-067	AGGTGACCGTACTGATAATAGAAGAGGCAGGGAAAGAGAAATCAATGATAATAGAA
			GAGGCAGGGAAAGGGAGATCAATGGCATCATGCTACTTCTTGTAGCTGTTTAACCT
			TAGTGATGTAATCTTCCATGGCAGACTCGGGGGTTTTATCTTTAAGTTGAATTTCCA
			TGCATCCCCTTGGGCTCTGTCCTCCAGTTGAATATCCTGGAACAAGAGGTTTTGCT
			TTCCACGGTCCCCT
SEQ ID NO:137	Late	LPZ-069	AGGTGACCGTGAGAAGGCAACTTTATCCCCTGCTAAACCAAGTCCAGAAATGAGGA
			AAATATGTGAAAACTGAATTGCTATATATGATGCCTAGTCTTGGCCTCTCAATTACA
			AGTTCAACGTCTTCAAATGATTGAAATATGGACCTTCTTAACCGTTCTGGAAATCTA
			TCAATCTTCAAAATTTTGAAACTTTGCCTCGATCTTGGAGTGATCAGACTTGATTTCT
			AATCCTAGAAATACCCTATCACTGGCTACCTGGTCTGTACGGTCACCT
SEQ ID NO:138	Late	LPZ-070	GGTGACCGTGGGATAGGCAGAAGCAAGAAACACAGAAGTTCTTCCGGGAATGTAA
			GCGCTGACAGTGGGGGAGAAAGTAGTGAACAAGGACATGGTCGGTATGAAATACA
			TGGCAGGCGATGGATTTCAAGGGATTAAGCATCTCAATGGATATTTACTATTGGAC
			TGTAGTAACTTTCGCCATCGCTTTTTGAACACATCTGTGGCTTAACTGTCATCTGTA
			ATGGTAAGCGAACCAGGTTTTGTTCTGAACCACTTGTATGTACGGTCACCT
SEQ ID NO:139	Late	LPZ-071	AGGTGACCGTGGTGGAGCGATTAGTGATTGTGATAAAGGGAGCATCAATATCTATG
			TAGACGCCGTATAAAGGTGGAAAAGGTATGTTTTGCAGGTATTTCTTTGTAAATGGT
			TTATAATGGGTTAAGCTCGGATATATGAGGTTTATATATAAGTCCTGTTAGTGTCAG
			TCTTACCAGCCTTCCTCCAGTGATCAAATGTGCTCTAACAAAGTGATTTTGAAGTGT
			CAAGGTCAAATTATGTCATTTCAGTGAGTCTTCAAACAAAATTTGGTCACTAGGCAT
			TAGGTCTAAGGGTTTGCTTGAACTCCCTCTAGAGTTGTCCAAATGGGCGGGCTATG
			TCATCATTTAAGCTGAATCTATCATCCAATCAATAAGGTTTTTCATTATCATGTCAGT
			GTCTAAATGAGTCATTTTACCGTCTTGTTCACGGCTTCACTTGTGCCTTTGGCAAAT
			TCAATTCCCTCCTCCAAGGGTTTGAAACCAATTCTCTTGGACGGCCCCTAAACCAA
			ATCTGCAAAATCCAC
SEQ ID NO:140	Late	LPZ-072	AGGTGACCGTGGTGGAGCGATTAGTGATTGTGATAAAGGGAGCATCAATATCTATG
			TAGACGCCGTATAAAGGTGGAAAAGGTATGTTTTGCAGGTATTTCTTTGTAAATGGT
			TTATAATGGGTTAAGCTCGGATATATGAGGTTTATATATAAGTCCTGTTAGTGTCAG
			TCTTTCCAGCCTTCCTCCAGTGATCAAATGTGCTCTTACAAAGTGATTTTGAAGTGT
			CAAGGTCAAATTTTGTCATTTCAGTGAGTCTTCAAGCAAAATTTGGTCACTAGGCAT
			TAGGTCTAAGGTTTGCTTTAACTCCTTCTAAAAGTTGTCCAAATGGCGGGCTATGTC
			ATCATTTAGCTGAGTCTATCATCATCATAGGTTTTCATTATCATGTCAGTGTCTAATG
			AGTCATTTACGTCTTGTTCAGCTGAGTGTGCCTGGCAATTCATTCCTCTCTAAGGTT
			TGAACCATTCTCTTGACGGCACTAAGCCAATCCACACTGGGGCCGTCTATTGAATC
			AACCCGGACACTGGGTTACAGGCAAC
SEQ ID NO:141	Late	LPZ-073	AGGTGACCGTCCAAGAAGAAATTGGCTTCAAAACCCTAGGAGAGGGAAATGAACTT
			GCCAAGGCACAACTGAAGCATGAACAAGACGTAAAATGACTCATTAGACACTGACA
			TGATAATGAAAAACCTATGAATGATGATAGACTCAGCTAAATGATGACATAGCCCGC
			CATTTGGACAAATTTTAGAAGGAGTTAAAGCAAACCTTAGACTTAATGCTTAGTGAC
			CAAATTTTGTTTGAAGACTGACTGAAATGACAAAATTTGACCTTGACACTTCAAAATC
			ACTTTGTAAGAGCACATTTGATCACTGGAGGAAGGCTGGAAAGACTGACACTAACA
			GGACTTATATATAAACCTCATATATCCGAGCTTAACCCATTATAAACCATTTACAAAG
			AAATACCTGCAAAACATACCTTTTCCACCTTTATACGGCGTCTACATAGATATTGAT
			GCTCCCTTTATCACAATCACTAATCGCTCCACCACGGTCACCT
SEQ ID NO:142	Middle	LPZ-074	AGGTGACCGTGATAGACCCCAAGAAAAATAGATCCAACCCTCAGAGGGACAAAGA
			CTTATAAAGACTAGAAGAGTGAATCAACCTATTCTATTTAGAATATATATTTTTGGGG
			TGCTTGCTTATCGTTTTGGGGGTTAATGTATGTCGTACTACGGTCTTATGCCCTAAT
			TTGCCCATTGAAATCAACTAAATTGACAGTAACCGACTAAAAGTTGGTCCACACTAA
			GATATCGATGACCAACGATCATAAAGGTGTCCATGATCCTAATAGTATATGTGTCAA
			TTAATGTAACTTTGGTGCTACAACATAAAACCATTCGTGGGGATCCTCCTTTTTATG
			CGGTCACCT
SEQ ID NO:143	Middle	LPZ-075	AGGTGACCGTGGGACCGACCTTGACTACAGGCCAAAATTTTGACTGTTGACCAGC
			GTTCACTTCTGTATTTTTGGTTGGTATGAGCAACATTGACTTGCTGGAAATTGACCA
			GGTTTGACTGGTATTTGGACTTGGATTTTGGCACAGATTTCTAGACAATTTGTATTT
			GTAAACCTTACAGAAGAATAATTTATCGAAGAAGAAAAATGCTAGGTTTCCCCTCAA
			GTTTGGGTTTCCCAAGGGAAAAATTGTTGTCCCAATGGTTGAATTTTCCAAAGGTCT

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			CCTAACCCGACAATACCTCCTAAGAATTCCTTAATTTAACCTTTCTTGTTTTCACGGT CACCT
SEQ ID NO:144	Middle	LPZ-076	AGGTGACCGTGAAGGAGCAGCAACAATTTGATTTTGTTTGGGTAGATCGGGGATTT TCTCGTGGAACATACCTGATTGAGTATAAACTAAGTCAAGGTACTGTGCTTGAGAAA TTACTTGCTCCTCAGTAACTACTCTGGCCTTAGCTACATCCTCAGTGATCTTGGGTA GTAAAGATTTTACAAACCATTCAGCTAAGATCTGATCCGGGATATAAACTTTCACTA AACGTCGTCGACGTCTCCATTCATGGATATGATCTGAAATGTAAGTGGACGTTGAC TGCTTTAACGAAGTTAATAATTCTGTGCCATTTTCATATCTGACGGTCACCT
SEQ ID NO:145	Late	LPZ-077	AGGTGACCGTACCTAATGGGAAGACACTTCAAGGTAAAAACAAATCATGATAGTCT TAAATACCTTTTAGAACAAAGATTATATTCAGAACAACTTGCTGGAAGTGTACCAAG TATGACTGGTATTGAGACTTAGATCTTCGCACAGATTTCAAGACAATTTGTTGTTGT AAGACTCACTCACGAAAAGTGATGTGGATATGAAGAACTTCCCTGTCGCCTCTTGG TTAGGAGTCTCCCACTCATAGGAATTGTGTAACTTATAACTTGGTCCACTAAAGAAG TTAGGTACAGTGTGTTCCTTTACCAGGTTCCCTGTTGTAACTTACAAATCTACGGCT ACCT
SEQ ID NO:146	Late	LPZ-078	AGGTGACCGTCACTGGAGGTTTGAGATGCTTGATCGGTACTGAAATGAGACATGAT CAGAATAGGACCTTGTTGAGGCCGTGTCTCACCCCCCATCCACAATCTTTTGTAAT TTTGAGTTTCGTTTAGAACATACTTGTAGGATAAAACTTACCTTACTCATGGATCAT GGCTGTATATGTTTATCGACCAGAGACAGATATGCCGAATGAAAGCGAGTCTAGTA TTCTAATGCAATATATTGGTAGTATGGGACATAGTACTGAACACTTGTATAGTACGG TCACCT
SEQ ID NO:147	Late	LPZ-079	AGGTGACCGTGGTCTCAGTTATGCCATATGTCCGCCCCTCCATATGATGCTCCGCC TCTATGGGGGTCTTTGCGATGTTGATATCTAGTAGTACTTCTTGTCCTATTGCAGCA ACCTGTACTGGTGTTGGTGTTGGTTATGGGTCTCCTACGCGATGGAGATATGAGAC ACCCATAGGTCGAACAGGTCTAATATCTGGAATCCAACGCTATTTGTTGTAGAAG ACGTTGCTCCCGTCCTTTAGCTTTGGCTGGTCACTATCCTTACGCTCCACGTACGG TCACCT
SEQ ID NO:148	Middle	LPZ-080	AGGTGACCGTTGGGAAATGCAATACCTCTCGTCCAGGTATATTCAACTTGAGGGAC AGAGCCAAGTGGGATGCATGGAATTCACTTAAAGATAAAACCCCCGAGTCTGCCAT GGAAGATTACATCACTAAGGTTAAACAGCTACAAGAAGTAGCATGATGCCATTGAT CTCCCTTTCCCTGCCTCTTCTATTATCAGTACGGTCACCT
SEQ ID NO:149	Late	LPZ-081	AGGTGACCGTCAAGGCAAAGTGTCATGCCACTCATTGGAATTAGTTAATATAGCTA ATTTGAGATATTACAGTCAACTGTGGGTATATGTATGTGAGATCAAGGTGCAGTTTA GATATTATCAGTGGTGCAGTTTAGATATTATCAGTGTTTGTGAATCTGCATACTGCT TTTGGTTGGTTCTAACTACGGTCACCT
SEQ ID NO:150	Middle	LPZ-082	AGGTGACCGTAGACATATATCATGGAAAACCCAAGTAACATACAAACACAAAACACA TGGAAACTTCATAAAACCTCCACTCGTCATAAGCTTTATTGCTATGTTATTGTGGTG TTGCATCGTACTTAGTGGAGGTTATTGTTATGTTATGTGTTCTATTTTCCTCCCGAA CGCCCTTCGGAATTGAGCTAACCGTGGTTAACAACATGTGGGCTTTTTTTCTCGAC AGTATATATATAATAAATCTTTATTTTTTTAAAAACTAATGCTATTGCATTTATATACT GGAAAAAATGATTTTTCTTGTATTATCGAAAATAATAATTTAGTTTCTTGATAATCACT TGGAATTAAGAAATTACAAACCCTAACAACATCAAGAAATTTTAAAACACATAAGCTA GAAATTTTAAAACACATAAGCGTGACAACAAGAAGATCAAATCTAATACTTGCTTGG GCCGGAGATTATGGATTCATGAAGCGATTTGACAGCGTCCATTGATCTTCCTCTCC CACGGTCACCT
SEQ ID NO:151	Late	LPZ-083	GGGGGTAGGGGTGTTTATACTGAGCATACTTCGAAAGTGGTTCACCACCACCATGA TGACTAATTGTTCCTGACTTTGGTAGACCTATAATAAATTCCATAGAAACCTCCGTC CATATTGATGCCGGAATGGGCAACGGTTGTAATGTGCCTGGTACTTTGACGGTCAC CT
SEQ ID NO:152	Middle	LPZ-084	AGGTGACCGTTGGGAAATGCAATACCTCTCGTCCAGGTATATTCAACTTGAGGGAC AGAGCCAAGTGGGATGCATGGAATTCACTTAAAGATAAAACCCCCGAGTCTGCCAT GGAAGATTACATCACTAAGGTTAAACAGCTACAAGAAGTAGCATGATGCCTAGACA AATAGCTTTGCTCAACACATCCTGATAGTGTACACTAAATCGCACAACTTTACTACT ACAAAGAAAGATCGTTGACACCTTGACAAATAGCTTTGCTCAACACATCCCAACAAT TTGGATTGCGAATACCGACTCCAATTTGTACTTGATCCATATGTCGTTGCGATGTAC TAGTTCCTCTATACATATGTTTCTGCAAGAATCGGAGTTGGACCTCTTCTTCCCTGT TATCAGCACGGTCACT
SEQ ID NO:153	Early	LPZ-085	AGGTGACCGTGGATAAGAGAACGCTTTGCCGACTCTCTGGGATGCCCTTCCCTCC ATAGCCGTCGTGGGAGGACAGAGCTCCGGGAAATCCTCTGTGCTGGAGAGCATCG TTGGAAGGGATTTTTTACCGCGTGGATCAGGTATTGTTACTAGACGGCCGCTTGTC CTTCAACTTCACAAGACTGATGAAGGCAGCAGGGATTACGCCGAATTCCTTCACCA ACCCAGAAAGACATACACCGACTTTGCACTGGTAAGGAACGAAATTGCGGATGAGA CTGATCGAATTACATGGCGTGCCAAGCANAGTCTCAAGTGTCCCAATTCACCTTAA TATTTATTCACCCAATGTTGTTAATTTGACTCTAATTGATCTCCTGGGTTGACAAAAT TGCTATTGACGGTCACT
SEQ ID NO:154	Middle	LPZ-086	AGGTGACCGTTGGGAAATGCAATACCTCTCGTCCAGGTATATTCAACTTGAGGGAC AGAGCCAAGTGGGATGCATGGAATTCACTTAAAGATAAAACCCCCGAGTCTGCCAT GGAAGATTACATCACTAAGGTTAAACAGCTACAAGAAGTAGCATGATGCCATTGAT CTCCCTTTCCCTGCCTCTTCTATTATCATTGATCTCTCTTTCCCTGCCTCTTCTATTA TCAGTACGGTCACCT
SEQ ID NO:155	All	LPZ-089	AGGTGACCGTACATACAAGTGCTCAGTACAATGTCATATACTACCAATACATTTGAT TAGAATACGAGACTCGCTTTCATTCGGCATATCTGTCTCTGGATGATAAACATATAA AGCCTTGATCCATGAGTAAGGTAAGTTTGAAGCTACAAGTATTTTCTAAACGAAGTT CAAAATTACATAAGATTGTGGCTGGGGCGTGAGAAACGGCCTCAACAATGTCCTGT TCTGATCATGTATCATTTCAGTACCGATCATGCCTATCATACCCGCCTGGTGACGG TCACCT

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:156	Middle	LPZ-090	AGGTGACCGTACTGATAATAGAAGAGGCAGGGAAAGGGAGATCAATGGCATCATG
			CTACTTCTTGTAGCTGTTTAACCTTAGTGATGTAATCTTCCATGGCAGACTCGGGG
			GTTTTATCTTTAAGTGAATTGCCATGCATCCCACTTGGCTCTGTCCCTCAAGTTGAA
			TATACCTGGACGAGAGGTATTGCATTTCCCAACGGTCACCT
SEQ ID NO:157	Late	LPZ-091	AGGTGACCGTATAGTGTCAAGCTTTTCTGGATTGGATAATGGACGGCGGCTTGCGA
			CATACATCTACACATTCTGTAACAAGTACACTCTACTGCAACAGCAGACCCAATTTC
			ACCTCTTCAGTCAGCCAGAGATCTCGATGGATTTGGGTTGAGGAGGTTGGGGTTCT
			GCCTGCTTCGGCACGGTCACCT
SEQ ID NO:158	Early	LPZ-092	AGGTGACCGTGCTAAGTAATTATCATCTGTACCTGTGCTTGCTGCAGGAAGTAAAC
			CAACCCGACTAGTCTTTTTAATAATACAGGGAGCCTTGCCACCAATTTCCTCTTGAA
			GCACCCATATTGGACGGGTTTGTGTCATCCTCTGTATTATCCTTTTTCATCCCAAGC
			AGGCTGTCTGTTTTTGTAGTAGAAGGATCACAACACAGATCAGGCCCTCCATAGTA
			CAAAGAAGAACCGAGGAAAGTATCATTAACGTTCTGACTCCTGCCATGAAGGCTTC
			CACTATGACCTTGACCCTTTTGTGAATTACTGCCATTTAGACCTTGACTGGCTCTTG
			CAACCAAATGCCCCAGAATGGAACTTCTTTGTGCTCCAGTTCCATTGTGGTTAGTT
			GAATCCCTACCACGGTCACT
SEQ ID NO:159	Late	LPZ-093	AGGTGACCGTGCAATATTGTATTCCAGGACCAAGTACTTAGGACAGAATCAGGTCA
			CGAGTGGCTCCACTCCACAATACGATGTTCATCGTTTTAATCACAATACAAGTTTGT
			TAGTCCAAGTAAGTGCGCTGCTGCAGACAGTGGGGCACCCCCCGTGGGCTTTGAC
			TGCCTGTCATACTGTTCCCTCCTTGCTCCTGCTCTTGCTCTCGCTGGGCTGTGGTG
			AGTTACTAACCTGGTTCGACCCACAAGGGCTTCTCACTAGGGCGTTAGGCTGCATG
			GATCTGCCAGATATTGTGGTTGCAAGGGACAGAGGCATGAGACACAGGCCTTTGC
			TTTGCAGAAACTGCATTGCTGACCCCATGTTTTCATCCATCAGTTTTGCTACCTCTC
			CTTCTGTTATGGACGGTCACCT
SEQ ID NO:160	Late	LPZ-094	AGGTGACCGTATCCGCAGCAGCAACAGCAGTAGAGCCTGAAGCAGGGGACCTAAT
			TACAGTCAAAAGTCCAGGGCTACCAATGCCTGCTAACAGCGCACTTACTTGGACTA
			ACAAACTTGTATTGTGATTAAGACGATGAACATCGTATTGTGGAGTGGAAGCCACT
			CGTGACCTGATTCTGTCATAAGTACTTGGTCCTGGAATACAATATTGCACGGTCAC
			CT
SEQ ID NO:161	Late	LPZ-095	AGGTGACCGTATCCGCAGCAGCAACAGCAGTAGAGCCTGAAGCAGGGGACCTAAT
			TACAGTCAAAAGTCCAGGGCTACCAATGCCTGCTAACAGCGCACTTACTTGGAACT
			AACAAAATTTTTATTGTTAATTAAAAACGAATAACATCGTTTTTGTGGGAGTGGAACC
			ACTCGTGAACTGAATCCTGTCCTAAGTTCTGGGTCCTGGGAATAACATATTGCACG
			GGTCACCTT
SEQ ID NO:162	Middle	LPZ-096	AGGTGACCGTTACAGCTAGGGAAGACTTTAAAAGTTTGTAAAACTAAGCATAGCTCT
			TAAACACTGAAGTTAAAAGACATGATTGGAATGTGCAAGTGGTTCAGTATCCAAATA
			TTGAAGGTTGCAGAATATGGAGCTACTGTGCAAACGAGTAACTTTATCTATATTTTC
			ACAAGATCATACAATGGGAAACGTTGAGATAACAACTGCATCGGTGAACCAGAATA
			GTTATAAAAGTTCTTGCAAGTAAAGGGATGAATAATTGCATGGTTGGAATTAAGAAT
			GACCATGTAGAGCTGCTATACAGATTCTCCAAGGTTTTATATTTGAGGAGTGCGCG
			CTATTGATGTTGTGCAAAAATTTCAGAAATTAAGTTCTGCGGCATTTATCAAGGTTG
			TTTGAGCCATTTAAATAGCAAGTTTTTGTTTCTCCAAGTACTTTCAGGAAAGCAGAT
			AGCTCTAGTTATAATGCTCCAGTGACAAACACATCTAGTTGGGGCAGTGAATGACG
			CTTTTGTCATTCTCTTTTGGTTTCAGGCACGGTCACCT
SEQ ID NO:163	Early	LPZ-099	AGGTGACCGTGGACAAACTCTAGAACAGGCATAGCTTTCATGTTCAGTTGTTTTTAA
			AGAGCAGTCCTCGCAGCAGATGGTGCAGCTTCCTGCTTCACTTCCGTTGATTTTCC
			TGATCTGAAATACCCGTAAACTTGCTGAAAGAACCCAAATACTTAATAGCGTCTCTAA
			ACAAAA
SEQ ID NO:164	Late	LPZ-100	AGGTGACCGTGCCTGAAACCAAAAGAGAATGACAAAAGCGTCATTCACTGCCCCAA
			CTAATGTGTTTGTCACTGGAGCATTATAACTAGAGCTATCTACAAGCCAAAACAGTG
			TTTGGGAGAGATTCCATAACGTCATTGCCTCTGCTACACATCATTCATTGGTTCCAA
			TAATGAAGCCACGTGCTAAGGACATTGAGAGAATCTTATAAAACAAGAAATATAGTA
			AATTGGGAAATGCATTTTATCGTCTAACCTGCTTTCCTGAAAGTACTTGGAGAAACA
			AAAACTTGCTATTAAATGGCTCAAACAACCTTGATAAATGCCGCAGAACTTAATTTC
			TGAAATTTTTGCAAACATCAATAGCGCGCACTCTTCAAATATAAAACCTTGGAGAAG
			TCTGTATAGCAGCTCACATGGTCATTCTTAATTCACACCATGCAATTATTCATCCCTT
			TACTTGCAAGAACTTTATAACTATTCTGGTTCACCGATGCAGTTGTTATCTCAACGT
			TTCCCATTGTATGATCTTTGAAAATATAGATAAAGTTACTCGTTTGCACAGTAGCTC
			CATATTCTGCAACCTTCAATTTTGGATACTGAACCACTTGCACATTCCAATCATGTC
			TTTTAACTTCAGTGTTTAAGAGTATGCTTAGTTTTACAAACTTTTAAAGTCTTCCCTA
			GCTGTAACGGTCAC
SEQ ID NO:165	Middle	LPZ-101	AGGTGACCGTAAAATACCATGAGAAATGCTTTCATCAGGCACCGCTGGTAGGTTTT
			CTTAAGCTTTTCATTAGGCAAAAGAGGCTCCGTGAGTTGATCGTTAATTCTCTCCTT
			GAATGCCATATTGACCAGACACTCTGATTAGAAACTGGAATACAACTGCACATATAG
			TCATTCTATATGATTCATCCTTCTGCACTTCAGCATCCTGCGGCAACTCTTCATCCC
			GCCATACTGAGAAAAATTATTTGACTCTTGATCATGTGTAGATGAATCTTCATGAAT
			CTTCTCATCTTCATTCTTGTCTTTATATCTTTAGGAAGTGCATCTGGTAAAAGTATAA
			ATGCATCTTCACGGGTGCTTCAGTTTTTGCATGCTCCCGGTTCTTCTTGTTTAGCAT
			GTGGATCTAGCAAATCACTAAATGTAGTTCTCTCAATTGGTCTGGTGGAAATTCTCC
			TCAATTCGAGAATTACGAATCATCATACCTGAGTAATATATGTTGCCCTGTACATGC
			ATATGCTGGTTTTTGGCTCCACCATTCTCCAAAGGGCTCAAAAACTATGCGACCCC
			TGGTTGCCGTAGTGGAAGGTTATACATTGCGTTCCCAGTAGCCACGGTCAC
SEQ ID NO:166	Middle	LPZ-102	AGGTGACCGTGGAGGGGCTCCACTTATATGCATAGATGATGCTGCGAGGCTGTGT
			TCATCTGGTCCAATGGAGAAGGGGAAGACCAAGTGCCTATCCTGATTTTGGTGCC
			GCTTGTTCTGGTGTACAGAATATCAACCCAGGGTATGTACCATCACTTCGTGAGAC
			GTTCACATTTCCCCACTTCTTGGTGGAGCTGGTGGAAAGCCTGGAACTTCATCAAT

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			CTATCGTTGGTGTGAGGATGATCAGGCTCTGTACTTATATCCACATGTAGTGCAGC
			AGGTGGTGGAGATGTCTCTGATAAGTTGGGGGTTGATACTGGTTCGTATCATTTGC
			AGTGATGTTCCCCCGCTGCCCTTAATTGCTATTGATCCATCATTAACTATAGGTTTT
			TACTCGCCCGGAATAAGACAATCTTTTGACACTTGTTGCTTGGGTCAC
SEQ ID NO:167	Early	LPZ-103	AGGTGACCGTGGCGCCTGACCTGTGCAGAATCCATTCTCATGGATACAATACTGTT
			AAGTTTGCTTTGCTTTGCTTGAAGGATCTGAATTGAAAAATTGTCCCCACAATTCTG
			TTTCGTTAAAAATGACCTCAATCACTCTCGACAGTTTCCAGATCTTGATTGGGAGCG
			TCCTCTCCTCTCTCAAGATGTTGTTGACCAAATTCAGGGCGACTTGTGGCCAGAAA
			TCGTACATTCTGCCATCTACCTGTTATTGAGCTCCCCGATTTATATGCGCTTTTGAC
			GGTCAC
SEQ ID NO:168	Middle	LPZ-106	AGGTGACCGTCAATACCATTAAACTGGGGATTCGTCTCAACAAGTCAACATGCTAA
			CCTCACAGCTCCAATCAAACAACGTCCGTCGAAGGGCGCTCACACTCATCCAAATT
			ACTTCCCTCTGCAAGACTCACAAAATCAGATTCTTCATGAATTGCTCAAACGAGGCT
			GTTATGGATGATGCAGCTGATTACTCAAGTGACAGCACTCTGAATCCCCGTCCCAT
			ATATAGCGACGCGGCGTTTCAGCCGTGACTGGTCGCAACAGCCTCAGTGGGACAA
			AAGGCCAGAAGCCCCCCAAGGTTCTCACGGTCAG
SEQ ID NO:169	E,L	LPZ-107	AGGTGACCGTGTCGATGTTGTTAGATGTGATTAGGGTTTTATTTCTTGATACAGATG
			CACTGTTTCTGTGTTTATTCTTTTATTTCTTCAATGTATGTTGTCAAATTATACTTAGT
			CA1GATCTCCTTTTATCGTTCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG
			TTTAACAATTAAAAGGGGAAATTAGGCCATATCAGCTTGTCGTATGGACCCACATGC
			ACTGTAGGTCAC
SEQ ID NO:170	Middle	LPZ-108	AGGTGACCGTATGCAGAGTCAAGGTTTAGTTCCTTCAGAGCCTGCCCGAGTAGCA
			CTGAGGCAGCTCAAGCCATTTCACGTAGGAAGCCCACAACAAAATAGAAATCAGAG
			TGAGTCTTTGATCGAGTAACCCATAAGTTCTTAGCTCCCGTTCCATCTTAACATAAG
			CATTTTTCTTGGTCTTCTCGCAGCCGT
SEQ ID NO:171	Late	LPZ-109	ATTGCAGAGGACTTAGAGAGGGAAAACCGTTCCGATCTGGTGAAGCAATTGGATGA
			AGCGCTCTGGAATTGATTCCCGTTTCTGATGATATCGTACGGCTAAGCTCAGCTCT
			TCAGGCATTGGCAGACAATACGATTCTTCAAATGAGATGACAGATTTTAAGAAACTT
			ATAGGATGACATATTTCCTAGCTTGAAGCGGATTCCCCCTACGGTCAC
SEQ ID NO:172	All	LPZ-110	AGGTGACCGTCCGATAAAGGATGAGAATATAGGTAGATCAACCCAAAAACACTCTC
			AGAAAACGATTAAAGCCTAACCCCAAGATCGTTGAGTAAATTTAACCCGGTAACCTC
			CACATAAATATACTTAGCAACAATAAACTCAACAACTAAACTATCCCTTTAAAATTA
			AATTATCCTTATTTATTTAAAAAAACAAATCCTTTATATACTAAGGTCCCCTGCACAT
			CTATTACTAAGGTAAAGGAAGGGAATTATATGCTATCATTGTAAACTTTGACTTCCG
			TATTTATGATCAGACCATGAGTTTGATAATTAATTTTACGCTCTTTACTCCCCATTCA
			AGGCACGTGCCTGGTGATATATGAACGCCAAATTATT
SEQ ID NO:173	Late	LPZ-111	AGGTGACCGTAGAATACAATCTATGTATCAAAATGCTAACAAAGAGAATTTGTTGTC
			TAGCTTGTAAATATACAAAAGAAACTCTCACAAGGAGTGAGAAGCACTAAGGCCCT
			TGGAAAGAATACGTTTCTATTCAGCGGAGTGTATTTTGAGCTACGGCTTGGCACAA
			CTCATCCTATAAAACAAGACTCTGTGAGAGGGCAGAGACCTTGATCCTGGGCGTG
			GCAAGCCGGGTGGCTATTGCGGTAAATCGAGAAGGGGGACCCTGGAAAAGAGAG
			GCTGAAATTTGTTTCATTCTGCAACTGAAACCTAACCGGAGGCCGAATCTGATCATT
			TCTAAGACCTTTGGGGTCCTGGGCATCCCATTAAAAGAACGCTGCTAACTCTCCCC
			TCCACAAAGGGCCAATGCGCTCAGGTCGGGCTTCTCATCTTCACATTTCTTGCCGA
			AATCTATCTGAATTTGTTGTATTGAATAACACTGCCTCCTACACGGTCAC
SEQ ID NO:174	Late	LPZ-112	AGGTGACCGTGGGCGCCGTGGCTCAAAAGGCCCTCGCAGACGCCCGCTCCATCA
			AGCTCATGGGCCCCCTCCACCCTCGGGGGGCAAGCCGGGAACGTTGCTGTCAGA
			CGAGGCGAGGACCTGGAACTGCCGTTGAAGGAACGGTTCTATATTCAGCCCCTCT
			CGGCGGACCAGGCGCTGCGAGAGCCAAGGAATCCGCGGAAGCAAATCCTGGAGG
			TGAAAAAGCTGATAGATAAAAGGCGTGGCCGTACGTCCAGAACGACCTCCGCTCC
			AAGGCTTCTTACCTTCGCTACGACTCAACACCGTTATCTCCTCAAAGCCCAAGGAA
			CAGAAAAAACCCCTCAAAACCTCACCCCAAAGCTTTTTTGACACCCTTGACAAACCT
			GGACTACGCTGCAAGGAGCCAAGGATACCCCAAGGGCAGAAAAAATACTTTGCAG
			AGCTGGTGAACCGCCCTTAATGATGTTCATTCCAAGCTTGGTTAAGCTGTATTGC
			ACTCATTGTTAACCACACTTAACGCCAATCCAATCTATGCTGTGTTGCATCTCCACT
			TCTTAGTTAATAACGTTCTGTGTTCCCAAACTCTGTGCCACACACGGTCAC
SEQ ID NO:175	All	LPZ-114	AGGTGACCGTACAATACAAATAGGTAGTTTATCACATTGTAGCTTATAGAATGTACA
			ATTGAAATCAAATAAATTCAACCAAACTCAAATAATATGATCATGTGCTCCTCACCTT
			CTCAGCAAACTCGTAGAGCAGAAAAAAGGATTATGTTAAATCACAGTTCACACATTA
			GGGTAAATCCCACTAAATGACCTCTCTTCATTATCCAAGTATCTGACACCAACATAT
			TTCAAACAAATAGTGCAAAAAGGAATGGTGAAGTAAATAGTCAAACTAAAAAATA
			AGCTTAAAATTTCTCACATGTTTGAATATGTGCACCACAAATTTTGTTAGTGTCATCA
			AAATGCATGTAATCAACTTGCCGTGTATATAATTTCACACAATATCCGTAAAATTTTG
			CAATTCCTTATGAGCATTTCATGTCTAGAGATTGCAATGACTTGGCTACAAACATGT
			TTCTCTACACAAGATCACAATATTTAGTCAGGACACGAATTGCAATGGGGATTCTCA
			CAAGCATCACAAGTCATCTCCCATGTACTAAAAAATTGTTTAAAT
SEQ ID NO:176	Middle	LPZ-115	AGGTGACCGTATAGTGCATATTCAGATTGCAATTACAGACGTATTAGAACCAGATTT
			TCGCTTCGATACAGCTCATCGAGAGCAACAGAGATCCAGATCAAAAACCAGACACA
			GTTTAAGAACATCGAAATACCAAGCCCAGGGACAGTTACCAGCATATAGCTCTACC
			ACCAACAGATTATTACAGAACCAAAACATAAGACCACTTGCAGACAAAAATAAACCC
			TAACGCAGAACGTGGCAACTATCTCCTCCAGCTACCACCATCGGAACCACCACCAC
			CATAGCGAGAACCCCACCACCACCATAGCCGCCACCGCCACCACCATAACCACCA
			CCACCACCACCACTGTACCGCCACTACCGCCATAACCACGGTCAC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:177	E,L	LPZ-116	AGGTGACCGTCCTTGGAGATAGCAGCTTCAAAACCTCCAGTGGTGGAGTCGATGAT CAA1ACTGCACAGTCAGCCTGAGATGTTCCAGTAATCATGTTCTTGATAAAATCACG ATGGCGGGGGCATCAATCACAGTGCAGTAGTATTTAGTTGTCTCAAACTTCCAGAG TGCAATATCATTGTGATACCACGGTCAC
SEQ ID NO:178	E,M	LPZ-117	AGGTGACCGTATAGTAGGAACTTTAGGTGCTTTGGTGGCACTCTCCAATTTTCATG TCCTTACATACCCCACTACGGAGAAGGGTAGCCCAAGATTTGAACCCAAGACTTCC GGTTCGTGAGACTTCATTTCCACGGTCAC
SEQ ID NO:179	All	LPZ-118	AGGTGACCGTAAGATCAAGAGCACAGAAAGCAGCCATAGCCCCGCCCATTGAATG CCCATAACAATAATCTGTAACCCATCTCTCTGTTTCTGAGCTTTCTGAACTGCTTCT ACAACAGTGGTCGTAAGGTTGTGTTGTGATAAGCAGAGTAAAATCCATAATGTACC ATTGCACCAGCATATTAGGATAGTTGAGATCAAGTGTCTTACAGAATAAATCCTCCA CCCAATTCTGTAGCTCCTTTCTTGAGTACCCCTGAATGCAATTACAATTGCATTGAT ATCTTCTGCCACACCACAAAAGCCTGAAGGCAGTGTTGTACATCAACTATAAGCTCT ACCACCTGAAAACCCCAGTCAAACCATTGCACCTAGAACAAGTCCAAGACATTAGA GCACTCAAATCATCCATA1AGACCGCAGAAGCATATTGCACAAGTATCTCAGCAAGT GTTCGATTATAGACATGGCCA1GGTCAC
SEQ ID NO:180	Middle	LPZ-119	AGGTGACCGTGGGAGGGGAGATTTTTGATTTATATTTCCAATATAAAAGAAAATCTA NGTTGTAAGGACATGGCAAGAGCTCTTATTTCCGGGGTTTTAGCCGTGGCCCGGA GCGGATGAAAGCAAATGTAAGTCACTCCGTGCTTTCTCGGCATTTGGACGCTTCTA CTCTACCGCACTACAGACGGGATTGAACCTCGCATCTCTGAGTGTTTGGTCGTTTA CATGGCGGACTTGTTCCGCACCTCTGCGGACGTCAAATGCCGCGACGATAATCCC TTTGAGAACAGCGATACGGCAGAAAGATCGCCGTTGACGAAGCGAGAAAACTATTG AGACTTGCAGATGTGGAGCTGAAGAAGAGCTTGAGTCGACGGTCAC
SEQ ID NO:181	Middle	LPZ-120	AGGTGACCGTCCGTTCGGGGTGTATTGTCGAACACGTAGGATGGTGCTACGTTGA AACCACCGTTACGTTCTTCGATATGTTATAGTTCGAGTTCATACGGAGGGAATACC GTTTGTAGTGTTATTCAGCACAACCCCGTCCTGATTAAACACCCCCGCAACCAAGG ACGTATTCGACGTTCGGTATTGTTTGACACACTCAAGTTATAACCCTGAATAGGCG CTACCCGAAGTAAGCATTGTACCAGTCGTTATTTTTGCCTTCGTATTGCGAAGGATT TTGAAATATATCCGGACAGGCTGCAACCGATCTTCATAAAACTCTTTCTTAAACTGA GCAAACTGAACAGCATTAGCATTTTGACCCGACCTTTCATCGGCACCTGCTGCACA CCCGCATACGTATTAAAGCTATGTTCGTCTGGCCAGGTTTGCCTTTTTTGGTTGTAA TCAGGACAACGCCGTTAGCCGCCCGCGATCCGTAGAGCGACGTAGAAAGCCGCAT CTTTCAGCACGGTCAC
SEQ ID NO:182	Late	LPZ-122	AGGTGACCGTGAAATATGTGGGAGATGATATGTGGTTTCCTGAATATTCACCTCTT GTGTAGAAAAGTGAGATCCTTAAGATGTTTTGCTAATAAGACTCTTAGGAATGTTGG AGCCCTTTCAGAATGCCATTTGAATAGATTCAAGGTGGTAGCTGTTGCCTGGGGCT GTTTTAGGGTTTTAGGCCATGCTCTGTAATTTCATTGAGTCAAAATTGGATTAACTG GTGTCTTTTACCTCATAATAGCTACTGCAGTATTTGTCGATATAGCTTCCCTATTTAT TGACTCTCCTTAGGTACGGTCAC
SEQ ID NO:183	Late	LPZ-124	AGGTGACCGTCCGTTCGGGGTGTATTGTCGAACACGTAGGATGGTGCTACGTTGA AACCACCGTTACCTTCTTCGATATGTTATAGTTCGAGTTCATACGGAGGGAATACC GTTTGTAGTGTTATTCAGCACAACCCCGTCCTGATTAAACACCCCCGCAACCAAGG ACGTATTCGACGTTCGGTATTGTTTGACACACTCAAGTTATAACTCTGAATAGGCGC TACCCGAAGTAAGCATTGTACCAAGTCGTTATTTTTGCCTTCGTACTGCGAAGGATT TTGAAATATATCCGCACAGGCTGCAACTGATCTTCGTAAAACTCTTTCTTAAACTGA GCAAACTGAACAGCATCAGCATTTTGACCCGACCTTTCATCGGCACCTGCTGCACA CCCGCATACGTATTAAAGCAATGTTCGTCTGGCCAGGTTTGCCTTTTTTGGTTGTAA CAGGACAACGCCGTTAGCCGCCGCGATCCGTAGAGCGACGTAGAAGCCGCATCTT TCAGCACGGTCAC
SEQ ID NO:184	Middle	LPZ-126	AGGTGACCGTCGTCAGAAAAAACGTGATTTCCGCAAACTTTGGATCACTCGTATCA ATGGGCAGCTCGTTTGAACGGACTTTCATACTCACAATTGATGCATGGTTTGAAGTT GGCTGAATCGAAGTGAACCGTAAAATGTTGGCTGACTTGGCTGTTAACGATGCAGC AGCTTTCAAACTCTTGCAGACGCAGCTAAAGCTAAGCTTGGGTAAATAATTAAAAAA AGAAGCGAGGTTTCCTTGGTTCTTTTTTATAACTTTTAATGAAAAGTATGAAGAGAG AAACAGCCTGTCTTCTACTTATAGTATAAGATAAAAGCTTGTTACTGATAAGACAGC TTTCATGGTAAAGCAGTTAAAAATAGGGATTTGCGATATAATAGAAAAAACAGACGT TTATGTAAATAAAAAACAGTAGAATGGAGAAATTATGTCAGAGAATCGTTTGGCTTG GGATCAGTATTTTGCGGCCAGGCTCTCTTAATCGCTAATCGCTCAACCTGTAAGCG AGCCAAAGGTGGCTCCGTATTGTCAAGGATAATAAGGGTTATTTCAACTGGGTACA ATGGCTCAGTTTCAGGGACTGGAGACTGTATTGACCAAGGAGTGCCTGGTCATTGA CGGTCAC
SEQ ID NO:185	Late	LPZ-127	AGGTGACCGTGGCGGAGGTTAGGGAAGTTTGACTTCTCATTTTCTCACGCACTCCT CTCCTCGTAACCTCGGTCGAGTCGATGGCGGCTTTTTAGTCGAGTGTGCTAACGC CCCTCCGGCCTCAAAATTTCCAGCTACTCGTATTTGATCAATGCTGAAATCGCGTAA TTACGTAGTAATAAAGCGTAATGAATTCTATAATGAAGCATGTTTCTCTATAGTTCAT GTGCCGAGAGGAATAATGAAAATGAGGCCTTATATATTATCTGGGGCTCAAGGAGA TGTTATCTTTTCCTTCCTTGGTTAGAGACCGTCAACCTTCACTTGATTGGATAAAGC TTCATTTTGTTAAAACCTCCAAGCCAGTAGATACATACGGTAGGCACGTATTATGGT AGAGACATACGGTCAC
SEQ ID NO:186	Late	LPZ-128	AGGTGACCGTCCTGTTGCCTAACCGCGAATCCAAATCGACTTGGGCTGCTTCCTTT CGTGCAGATATTTCTGGTTTGGACTCTAGTTCTTGCTCCTGGAAATCATGCTTGAGT GCTGGGTAGCTGCCTCCAAGTTTGGTTGACAGGCCCATTCCTTACAGCTTCTCTCT TCCGCTTATGACAGAGTAATGACAGGAATTCAACCTGACGGATCCGTCTAGCTCTC TGGATGAGCCCTCAGCTCTGTGTACTATTGTTCATGTACTGGATACTTTGTAAATGA TTTTATTCTGGTTTTACCCCGGGGGGGGCATTTTGACTCCTGGGTTTAATACGGTC AC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:187	Late	LPZ-131	AGGTGACCGTGGAACATGATGATTAGTTCTTCTGTGGGCCAGGATGATTAGTTCTC TGTGTGACTGTGGGCCAGGATGATTAGTTCTCCTGTGACGACTGTTGGATAGGATG ATTCGTCTCCTGTGGACAGGATGATTAGTTCTCCTGTCGAGGCACCCTACCCATGC AATTTGGGATCATGGGAAGTACCTCTCATCTGATCAATGAGTAGGGAAATGGGGTT AGGGACCATTAGAGTACTATCGATGGACACATCGTTGTATCTACCGTCCTATGCTA GGACGACCTCCATTGTTTGGGATTAGTGAGAGTGGTATGACACTCTGAGACTGACT TTGGGTCAGTGGAGGATGTATGATACATCCTCGATCATTTCTTCTTCTTCATAGTTC GAGCAGAGCAGAGCACAACAGGCCAAGTAGTGCAGGGTAGTGCATTTGATGGCTG GGATAGTAGCGACGGTCAC
SEQ ID NO:188	Middle	LPZ-133	AGGTGACCGTAAATAAGATGACCCACATGGAGTTTGGCCCTAGTTTCCAATTTTAA CAC1CGCTCTCAACTAGGGAGAACTCCATTCGCTGATCCATTTGTCCGACTATACTA TCTCTGCATCAGTGCCCTACACTACTCTGCACTGCTCTGCTCTACTAAACCATGAA GAAGAAGAATGACCGAGAATGTCTCATGCCATTCTCTATTGACCTGAAGTTAGTCC TATATGAAGAGA1TGTGTCATATCACTCTTATTGACCCAAAGTCAGTTTTATTGATCC CAGATCAATATCACAGAGAGTGTCTCAAACCACTCATACTGATCCCAGATCAGTTTC ATTGATCCCATATCAAGGAGATCATCCTAGAATAGGGAGTACAGTAGATACAATGAT GCATCCATCAATAGTACT1CTATGGTCCCTAACCCCATTTCCCTGCTCATTGATCAG ATGAGAGGTACTTCCGATGAGCCCACACTGCATGGGTAGGATGCCTCGACATGAG AAATAATCATCCTATCCACAGGAGACGAATCCTCCTGTCCCACGGTCAC
SEQ ID NO:189	Middle	LPZ-136	CTAGGGAAGACTTTAAAAGTTTGTAAAACTAAGCATAGCTCTTAAACACTGAAGTTA AAGACATGATTGGAATGTGCAAGTGGTTCAGTATCCAAATATTGAAGGTTGCAGAA TATGGGCTACTGTGCAAACGAGTAACTTTATCTATATTTTCACAAGATCATACAATG GGAAACGTGAGATAACAACTGCATCGGTGAACCAGAATAGTTATAAAAGTTCTTGC AAGTAAAGGGTGAATAATTGCATGGTGTGAATTAAGAATGACCATGTAGAGCTGCT ATACAGACTTCTCAAGGTTTTATATTTGAGGAGTGCGCGCTATTGATGTTGTGCAAA AATTTCAGAAATTAATTCTGCGGCATTTATCAAGGTTGTTTGAGCCATTTAAATAGCA AGTTTTTGTTTCTCCAGTACTTTCAGGAAAGCAGGTTAGACGATAAAATGCATCTTC CCAATTTACTATATTTCTGTTTTAAAAGATTCTCTCAATGTCCTTAGCACGTGGCTTT CATTATTGGGACCAATGAAGATGTGTAGCAGAGGCATTACGTTATGGAATCTCTCA CCAAGAACACTGTTTTGGGCTTTAGATAGCTCCTAGTTATAAATGCTCCAGTGACAA ACACATCCTAAGTTTGGGGCAATTAATGACGCCTTTTGGTCATTCTCCTTTGGGTTT CAGGCACGGTCAC
SEQ ID NO:190	Late	LPZ-137	TCCCTTTAGTGAGGGTTAATAGATCTATAGTGTCACCTAAATCGCGGCCGCTCTAG AACAGTGGATCCGCAAGCAGGATAGACGGCATATGCATTGGATGCTGAGAATTCG ATATCAACTTATCGATACCGTCGACCTCGAGGG
SEQ ID NO:191	Middle	LPZ-138	GGTGCGATCCTAAACATGCAAGCTTTGAGTTTGTAACTTTGTAGAAGTGGACATTTC TAAGTTGGATGTACAAATCTACTGTTGGTTGTATTGTCATCCCATAAACAACTGTTT GATGAGATGTTTTTTTAAAAACCACATCATAATATTTTTAGGCCTTGTAAAAAAAAAA AAAAAAAAAAAA
SEQ ID NO:192	Late	LPZ-140	ATTCCAAACTTTTCTTTCAAGATGTACACCAACATCATTGTCCCCAACTTAGTAGACT TGACTTTTCACCAGGTCCAAAGAGAGGGGTGGTGGAAGCAGATTTCAGGCTTTCG AATAAGTATCAATGATATAAGCATCATCCCCTTGCCAATTGTTCTGGATCGCAC
SEQ ID NO:193	All	LPZ-141	GGTGCGATCCCATCAGGGGTTGTGTTTCTAAGAATCACTTCCATGTTTCAAATTCAG CACTTGATCTTGTACATACCCAATTTGTTGCCTGCTACTAGCTAGTATTGTCTTTCA GTTTGAACCATTTTTTTGAGTAAATCGTGTTTAGTCTTTGGCAAAAAAAAAAA
SEQ ID NO:194	Middle	LPZ-143	GGTGCGATCCGCATTAGAGAAGCATACAGGAAAAAGAAGTACCTGCCTCTTGATTT GCGCCCAAGAAGACTCGTGCTATCAGGCGACGCCTTACCAAGCATCAGGCATCAT TGAAGACGAGAGACAGAAAAAGAAAGAGATGTATTTTCCAATGAGAAAGTATGCAG TCAAGGTGTAAGCCACAGGATTTGAGCTTTCATGCAATTTTTTTGTTACTTGCGGGA TGATATTGCCTATATATTTCCGTCCACGTTTTTGGCAAATTCCGATTTGCATCAGAA TTCAAGTTATGATAGTGTTCTTTCGCTTTTGAGCAGTTGATATTGTTTATCTTTTATT TCTCTTGAATTGCAACATATTCTAATGCAATGAGTGGATTATTATATTGTGGTATTTC CATGTTGAACTCATATAAATGAGCGTAATTTGAGTGGTAGCGCTAGGATATTTACAC TTGGCAAAAAAAAAAA
SEQ ID NO:195	Middle	LPZ-144	GGTGCGATCCGTATAGGTAGTTTGGATGATGAACGGGCAAAGAAGGCAAAGGAGT ACAGGATGGATCCTGTAATTCCTGTTTCAGAAAACAGAAAATCTGCAATATAAGGAT GGCTAACTTTTCAGCTATGAAAATATATGGTGCAGTGGCACTCATATCAGTTGCAGA GTTGTCAAATAACTTTTGTGAATAGGAAAGTTGTCCTCTTTTAGAGTGCAGAAATCC TGCAATATAAGATGGCTAAGTTTTTCAGCTATATGAAAATATATGGTGCAGCAAAAA AAAAAA
SEQ ID NO:196	Late	LPZ-145	GGTGCGATCCCATATACAATTACATATATTTTCAACAATTCTTTTGTTGTTATGAAAA TCTATTGAAATAAATTGAAATAGTTTGCATCATTTATTTATCGGAATTCGTATTTATAT ATTAAATTTCTGATGTCTCAAATCCTTCGTTACTGTAACGATATCATTAATATAATGT GTCTGCAAGTTTATTGGGCAAAACAAAATTTATTTTTCGGTCACATCATAAGTTTATT TTTGGTCACATCATATGCACCATCACATTAAGCATAAGCATATACAGTAGCGTAAAA ATACAATTATTGTTGTTGACTAGGATCGGAC
SEQ ID NO:197	Late	LPZ-146	GGTGCGATCCTAGTCAACAACAATAATATGTATTTTTACGCTACTGTATATGCTTAT GCTAATGTGATGGTGCATATGATGTGACCAAAAAATAAACTTATGATGTGACCGAAA AATAATTTTGTTTTGTCCAATTAGACTTGCTGTATATGTCTGGAGTCCTACCCTTGAA AATTGACTTGTTTCCC
SEQ ID NO:198	Late	LPZ-147	GGTGCGATCCCATATACAATTACTTATATTTTCAACAATTCTTTTGTTGTTATGAAAA TCTATTGAAATAAATTGAAATAGTTTGCATCATTTATTTATCGGAATTCGTATTTATAT ATTAAATTTCTGATGTCTCAAATCCTTC
SEQ ID NO:199	Late	LPZ-148	CCACTGCACCATATATTTTCATATAGCTGAAAAACTTAGCCATCCTTATATTGCAGAT TTCTGTTTTCTGAAACAGGAATTACAGGATCGATCACTGTACTCCTTTGCCTTCTTT GCCGTTCATCATCCAAACTACCTATACGGATCGCAC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:200	All	LPZ-149	AGAGCCTTCTTGCAGACAATCCGTGAAAACATGGCTATACAATAAAAATTCCCAGTT TGAATTCTAAAGAAAACTGTTCAATATTTGAAGGCCTCTGATATCACAGAGACTGAT ATTAAATGGAAATTCATACAAATGAGGAGAGCATGTAGCAACACTAGAAGCTTTGG CATAAAGCACCAGATAAATTCATAAGAACTAAATCCATAAGAAGGATCTCTCGTTCA CCAGTCACAATCACACTCGGATCGCAC
SEQ ID NO:201	Middle	LPZ-150	GGTGCGATCCCTGGCCCTGATAACTTTGGTTGCAATGGAAAATGCAGTACTAGGTG CGAAATGCTAAAGGCCGCCCGGAGCGGTGCATGAAGTACTGCAATATTTGTTGTAG TAAATGGCTGGTTGTGTTCCCAGTGGTCACTATGGCAACAAGGACGAGTGCCCCT GCTACAGAGAATGAAGTCCGCAGCCGGCAAGCCCAAGTGTCCCTGATCTTAGCAC TTCAGTGCAGTCGCCACTTCTTTTATTCTCTTTTTTTATAAAAGTGACGAGGCCGTTT TTCTTGTGCTTGGTGCCATATGTAGAGCGGTGGCTACTTCTCCTGTGTTAGGAAAT GTTGCAGTACTAATAATAGAACTTCTT
SEQ ID NO:202	Middle	LPZ-151	GGTGCGATCCAATAAAGATATACTTTGCAACAATAATCAAAATATCATTATGCAAAG TTTAAGATCAAAATAGAATGCAACAAAAAAATGGTTGTAACATAGGAACCAACAATG TTGCATTCAAGTAAGACTCTTTGCAAAAAAAAAAAATAAAAAAAAAA
SEQ ID NO:203	Middle	LPZ-152	GGTGCGATCCACAAGTAAGATAATTGAGTATATATTCAAGATGCAAATATTTCATTA GGACCACTCATAAAGTTATCAATGATTCACAAAGAGACCTCCTGACCTCTCTCAAAA GTGGTGGCAACACAAGACTAGTGTAGTTTTTACTATACCTCAATGAAACTACCATCC TAACTGATGCCATAATCTTCTGTTATATATTACCAAAATTTATGAGATGATTGATCCA TAAACACTCCAGAACACATAGTCATCCAAAGGAACCTTTGCTTGAATATGGACCCC CTTAATTCAGGTACTTGCTACTCCAATAAATTGCTTAATCTCTCCACCGATAACCAC AGTTTGGATCGCC
SEQ ID NO:204	Early	LPZ-153	GGTGCGATCCAGGACATGAGGCCGAGTTTGCCATTGTGATATGATTGAGGAAGTC CAGTCTCAAAATTAGGTTTATCTTGATGTTTGACAAGAAATATAGAAGGGCATGATG AATCAAGAACCTTTTCCAAATCTGTTACTGCAACCAATCCAATGACATAATAACGCC AATGGTTGGTTCCTGTGATGACATAATAAATTGGATTAAATTAATAACATCCCTAATG CCATGTGGTTAGCTGCATCATCACCGTATCCATCGAGTGTTCAATTTTTGGGATGTA TGTATCAAAAAAA
SEQ ID NO:205	Early	LPZ-154	AAATATTTTTCAATACAACGCCATGTGACATTTTTGTGCTTCTTGTTTTTGATACATA CTTCCAAAAACTGAACACTCGATGGATACGGTGATGATGCAGCTACAGCCATTGCA TTACGATGTTACTAAATTAAATCAATTTATTATGTCATCACACGAACCCAAACAATAG CGCTATATGTCATTAGAATGGTTGCAGTTACAGATCTGGAAACAGATCAATGAATCA TCATGCCCTCTATATCTCTTGTCAAACATCAAGATAAACCTAATTTTGAGGACTGGA CTTCCTCAACATATCACAATGGCAAACTCGGCCTCATGTCCTGGATCGCAC
SEQ ID NO:206	Middle	LPZ-155	GGTGCGATCCGTATAGGTAGTTTGGATGATGAACGGGCAAAGAAGGCAAAGGAGT ACAGGATGGATCCTGTAATTCCTGTTTCAGAAAACAGAAAATCTGCAATATAAGGAT GGCTAACTTTTCAGCTATGAAAATATATGGTGCAGTGGCACTCATATCAGTTGCAGA GTTGTGAAATAACTTTTGTGAATAGGAAAGTTTTCCTGTTTTAGAATGCAGAAATCC TGCAATATAAGATGGCTAAGTTTTTCAGCTATATGAAAATATATGGTGCAGCAGAGT TGTCAATATAAACTTGTGAATAGGGAAGTTTTGGCAAAAAAAAAAAAAAAGAAAAAA
SEQ ID NO:207	Late	LPZ-157	GGTGCGATCCTCGTTGTGAAGACGTAGTGATGGAAAGGTCATGTTTGTAGGAGAC ATAATTATAGGAGTTTCTTTATTATAATAACCAAGAAGTCCGATCCTGGGGGCGTTG AGTATATAGTCAGTCTTTGGTAATTTGGTGTGGTGCTGTTTGACCTGCCTTTCCTTT GGAGCAATGATCCTTGAGGATGGAAGAGGTTATGTTGAGGCTCAAGAGATGATTGT TTGAGTTGTGGAAAGCAAAAGGTTTCGAGATGTAGTCAGATAGTAACTTCTATGCTT TTAATAAAATTTAGTCTGTGGGGCATGCCCCTTTTTGCTGGCAAAAAAAAAAAAAGAA AAAAAAAAAA
SEQ ID NO:208	Late	LPZ-158	GGTGCGATCCGTATAGGTAGTTTGGATGATGAACGGGCAAAGAAGGCAAAGGAGT ACAGTGATGGATCCTGTAATTCCTGTTTCAGAAACAGAAAATCTGCAATATAAGGA TGGCTAAGCTTTTCAGCTATGAAAATATATGGTGCAGTGGCACTCATATCAGTTGCA GAGTTGTGAAATATAACTTTTGTGAATAGGAAAGTTTTCCTGTTTTAGAATGCAGAAA TCCTGCAATATAAGGATGGCTAAGTTTTTCAGCTATATGAAAATATATGGTGCAGCA GAGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
SEQ ID NO:209	Middle	LPZ-162	GGTGCGATCCCAGGAGAATATTAGTTTCATGTGTTGCTATCATTTTCTTCAATATGC AGGGCAACCATTTGAATGAACTATTCCTTTCGAATTTCAAAAACTTAATAGGCTAA CTTATCTATCTGGAGCCGATTTTCATTGACGAGTAACCTGTAAGCTGGCCAGCAAA AGCCAACAGATGTTCAGCTTGTTGGAACCAGTTGAAGATTGTAATAGAGATGGTGA ATAATCGCGGACGGCTCGGCCAATGGAATATTTGTTGCATCATCATCAAGGGGGTA TGAATTCCAAAGAACTTGTTGATTGAAATTCCCAAGCAAAATTCTGTGAAATGAAAA ATTTATTGAGACCATTGGGCAAAAAAAAAAAAAAAATAAAAAAAAAAAAAA
SEQ ID NO:210	All	LPZ-165	GGTGCGATCCGACTGTGATATGTGACTGGTGAACGAGAGATCCTTCTTATGAATTA ATCTGGTATCTTTATGCGAAAGCTTCTAGGGTTGCTACATGCTTCCATTCTAATATC AGTCTCTGTGATATCAGAGGCCTTCAAATATTGAACAGTTTTCTTTAGAATTCCAAA CTGGGAATTTTTATTGTATAGCCATGTTTTCACGGATTGTCTGCAAGAAGGCTCTTT GGCAAAAAAAAAAAA
SEQ ID NO:211	M,L	LPZ-166	TTTTTTTATTTTTTTTTTTTCCAACGAGATCACTGTCATTGTTCAATAACTATATGCCA AAGAGCCTTCTTGCAGACAATCCGTGAAAACATGGCTATACAATAAAAATTCCCAGT TTGGAATTCTAAAGAAAACTGTTCAATATTTGAAGGCCTCTGATATCCCAGAGACTG ATATTAGATGGAAATTCATACAATGAGGAGAGCATGTAGCAACACTAGAAGCTTT GGCATAAAGACACCAGATAAATTCATAAGAACTAAATCCATAAGAAGGATCTCTCGT TCACCAGTCACATATCATACTCGGATCGCACC
SEQ ID NO:212	Middle	LPZ-167	GGTGCGATCCGACTGTGATATGTGGCTGGTGAACGAGAGATCCTTCTTATGAATTA ATCTGGTATCTTTATGCGAAAGCTTTTAGGGTTGCTACATGCTCTCCTCTTTTGTAT GAATTTCCATTCTAATATCAGTCTCTGTGATATCAGAGGCCTTCAAATATTGAACAG TTTTATTTAGAATTCCAAACTGGGAATTTATTGTATAGCAATGTTTTCACGGATTGTC TGCAAGAAGGCTCTTTGGAAAAAAAAAAAATAAAAAAAAAAAA

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:213	Middle	LPZ-169	TCCCAAAGGCAATTATACATGGATCGCACC
SEQ ID NO:214	All	LPZ-170	GGTGCGATCCCCACTGCAGAAAGATGAGCCAGTACCCTGAAATTTTGCTGTTGTCC ATGCCTGGGTCACGGAGGAAAGAACGGCACGGTGCAATATGATTTTGCTACATACA AGTTCCAAGAGTGGATGCAGACAGTGCTGGCCATGGCTGATTATTTGCAGGTGACT AATGCTCTTTTGGTTATCCTTACCATCATCATCTTCCTGCCATTCTTTTGTACCTCGG TATGGAGACGAACACCCACTTTTCAAAGTTTGCAGAGGAAGCATGTATTCATAACA GGAGGATCAAGCGGCATTGGCCTTGAGATTGCCAAAGAGGCTCTTTCACAGGGTT CTTACGTGACACTGGCGTCAAGAAATCTTTCTAAACTTCGTAGGGCTGTTGAAGAA ATCATCCAAGAAGTGGAGTGCGACGGAGACAAGATTAATATCAAGGTAATATACCC TGCAAAATGTTGTCTGGAATACAATCCAAAACCAATTTAGCAATTAACCCATTGGCA AAAAAAAAAAA
SEQ ID NO:215	All	LPZ-171	GGTGCGATCCAAGTGCGGTATTCTTCCTTTGGCAGTTCTCTGAACTGTTGAGAGAA TTTGAGTAGGATAACGACAATAATTACTATGCTCAGAAGCCCAGACAACACGAATAG ACTCCCTTCCGTGCGTCGCCTTCCAGAGGACGCAGCAGCTAAAATCTCGGCCTGA CTCACCACATATATATTTAATAGCTTGTATATGCCATATGAACTGTTAGCATGATCTC CCTCTAACTGCGAATTGTGTTGCTGTAAACTAATCCCAAAGGATGTTTACTCTGTTG CTTTTCCAACTGCTGATGGATTTCGCTCATACAATGACCCGAGAGCACCATAAACCT ACCCAGCGTTGTGGCCTATGACCCATAGCTTTTTGTTCGCACAGCAATTGAAGACC GGCTACAGGAGATGACTAATGCACTTCCGAGAAGGTTTCACCGCGAATGACAGGG AAGGACAAGGCAGAGCAGCAGGCCAAGACAGCTTTAGTCGCAGAAGTTCAAGCAG ATCTAGATTCATAGTAAATGGAAGTTCTACACTAGTTACAAATTTAAAAACGTACCTG CATGGACTACACGGTTTATTTACGAGTGCCACTTGTCTCATTGTTTTCCATCAGATG TCTGCTGGATTGTGGTAGTGTGTTCTACCGTATCGGTGCGGGTTTTGTATATTGTG CGTCGACAGAGTGACAGGTGGTGATTTTACTGGCAAAAAAAAAAAACAAAAAAAAA A
SEQ ID NO:216	Late	LPZ-172	GGTGCGATCCTAGTACAGGCGTTTGGAACAGAGTGGAGAATATGTGGAGTATTGG GGGATGCGCCCGGTCGTGTGTTGCTGCGTTTGGGAATTTGTATTTCTTCCATAGGC AACAAGTGATGTCTTATAATAGTAAAGAGAATGTTTGGGAAGTGGTGGCATCTCTTC CTGGAGACATGAATATTGTTACTTTGCGCAACAGTGTGGTGTGACAAGATATTTGT GAGCGGTTGTGCTTGCAGTGGCGGCGATCAGGTGTGTTACATGCTGGACAAATCT TGGGCGTGGGCTCCTATTGAGAGGTCACATGAGTTTGAGGGTTTTGCTCAGTCTG CAATAACTGTAGAGATATGAGCAAATTCTGTTGGGTTCACTTAATTTTGGGATTATT ATAGTGCAGAGGGGAGCCGGGAAGTTTCAGTGTACAGTGATGGGCACCACATGTT GCCAGCATTGGGGGTGCCCTGTGAATATGATTTCTATAAGTCCGGATTTTAAATATC TAGGCCATCTATCTCATCCAGCCTCTGATTGTGTCTGTACTAAATATATCCTGTATA TTCGTGATCCCTGGTTTTGAAGTGAGCAAGTTTTAGTGGAAGAGGATTTTTATTAAA TATATATAAAGTTTCTGTATTCAGGGTTTTGGCAAAAAAAAAAAAAA
SEQ ID NO:217	Middle	LPZ-173	GGTGCAATCCGCCATAAGAGAGGCATACAGGAAAAAGAAGTACCTGCCTCTTGATT TGCGTCCCAAGAAGACTCGTGCTATCAGGTGACGCCTTACCAAGCATCAGGCATCA TTGAAGACTGAGAGACAGAAAAAGAAAGAGATGTATTTTCCAATGAGAAAGTATGC AGTCAAGGTGTAAAGCCATAGGATTTGAGCTTTCATGCAATTTTTTTGTTACTTGCG GGATGATATTGCCTATTATATTTCCGTCCACGTTTTTGGCAAATTCCGATTTGCATC AGAATTCAAGTTATGATAGGTGTTCTTTCGCTTTTGAGCAGTTGATATTGTTTATCTT TATTTCTCTTGAATTGCGAACATATTCTAATGCAATGAGTGGATTATTATATTGTGGC AAAAAAAAAAAAAAAAAAAAAAAA
SEQ ID NO:218	Middle	LPZ-174	GCGGACGCCTCAGGATAGCGTTAGGGTTGCCTTAGGATAGCGTTAGCTCTGCCTT CTAAGGTTGCCGTCTTATCCTCCAGCGTCTAGGGCTTCCACTCCTAGGATTTCTCT TCCACTAAAACCCAAGACAAGTGGAGAGAAATCAAGATAGAAGTGTGTGTGAAATG ACTCTTAAGTCATCTCCTTTTAGACTAAAACATTGAGCACATGTGGGGTTTATTTGG TTGCTGGCCGTCGTT
SEQ ID NO:219	Middle	LPZ-175	GGTGCGATCCTGAAACAACATATTCCCGATGGCTCTTCCGAAGGAACCATTGCTCT ACTGTGTGGCCCTCCCCCCATGATCCAAGATGCCTGCCTACCTAACCTGGCCAAAA TGAATTATGACATTCAGAATTCGTGTTTTCAGTTCTAATTACACCCTTCTGGTTAATC AAATTGGGACATCCCCTCCCACATCCTGTTATTAATTAAGCCATAGTCTAGTGTATA AAATCTGTTGATGTGTACAGCATCAAGTTAATTTCCTCCTTTTCTGTCAAAAAAAAAA AAAAATAAAAAAAAAAAA
SEQ ID NO:220	Late	LPZ-177	GGTGCGATCCGATCCTAAGCGGGTGCATATATATAATGACAAGCTGTAGTAACTAA CTCTTGTCATGAGGCCATTGCTAACATAGCCTGTCCAATGCACATAGCAGTCAAAA AAAGCAAATAGCCGCCATGTTCCCATACACGAAGTAAGTACCCTCCCTATTGAGTC ACCTTACCCGCCGAGAGAGATCCCAATTCCATGTATTCGGTTAAGTAAGCCCTGCC AGCTATGTCCCACCCATGAAAGAAAGTACTGATCCGAGTGGATCGCACC
SEQ ID NO:221	Late	LPZ-179	GGTGCGATCCAAACTGTGGTTATCGGTGGAGAGATTAAGCAATTTATTGGAGTAGC AAGTACGCTGAATTAAGGGGGTCCATATTCAAGCAAAGGTTCCTTTGGATGACTAT GTGTTCTGGAAGTGTTTATGGATCAATCATCTCATAAATTTTGGTAATATATAACAGA AGATTATGGCATCCAGTTAGGATGGTAGTTTCATTGAGGTATAGTAAAAACTACACT AAGTCTTGTGTTGCCACCCACTTTTGAGAGAGGTCAGGAGGTCTCTTTGTGAATCA TTGATAACTTTATGAGTGGTACCTAATGAAATATTTGCATCTTGAATATATACTCAAT TGATCTTACTTGTGGATCGCACC
SEQ ID NO:222	Late	LPZ-181	CAATCTGTCTGCAATTGATATTATTGCATCCAGTAAACCAGATACACATTCACCACA ACATTAGAGACTCTAGAAGTTCCTTTGGCGACAGGCAAAACTCATGATTACAGATAA TTGGAGTTTCCTCTAACCAGAGTCAAACGATCTAAAGGGATTTGTCTAGTCCTCCAT TCCCTCATTCAATGAGGCGATGGCTTATGCCGTGACAACAGTTTCTATAGTTGCAT GCGCTCCTCTTGATCCCACAACATTTTTGGTGTTCTCTGCATCTTCTTCCTCCCATA TCTCTGGCAGGGCTTCTCTAATGTTGTGAATACTTGCAAGGGCAAAATCTGCTCCC TCTGTTCGGATCGCACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:223	Late	LPZ-182	GGTGCGATCCTCTCAGTTACGAGCTCAATTTCGACCAGGGGTCTCGGCAAATTGA GGATCATGAGAAGCAGGGTATGCCCTTGAATGCCCTGAAGCCAGGGGAGTCTCAG GGCAATCACGAATGAAACCTGACAAACCCTAAGAAAACCCCTAGAGCGTGCCCTGC AGAAAGGGAATTCTTTTTGAGGCCGGCGGTCTTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:224	Late	LPZ-186	GGTGCGATCCAGCAAGAGAACGAAAAAGGTATGAGAATCTATGAAATATTTGTACA TCACTGTATTCATATGAGGGCCTTTTTTTACAATGCGGTAGGGTTGTTTGGAGAATT AGAACCTGATTAAAATGTAGATGGATTCAAGCTTTTAGTGAAATGAGGCTCGGAAC GCAAGTATGCTGTCCACTTTGAGACTCATTCTTCTATAGTATCTGAAGCCAAAGCC
SEQ ID NO:225	Middle	LPZ-189	GGTGCGATCCCATGGGATAGTTGCAAAACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTCACAACTCTGCTGCACCATATATTTTCATATAGCTGAAAAACTTAGCCAT CCTTATATTGGAGGATTTCCGCATTCTAAAACAGGAAAACTTTCCTATTCACAAAAG TTATATTCACAACTCTGCAACTGATATGAGTGCCACTGCACCATATATTTTCATAGC TGAAAAGCTTAGCCAGCCTTATATTGCAGATTTTGTGTTTTCTGAAACAGGAATTAC AGGATCCATCACTGTACTCCTTTGCCTTCCTTGCCCGTTCATCATCCAAACTACTAT ACGGATCGCACCA
SEQ ID NO:226	Late	LPZ-194	GGTGCGATCCTGCGAGAGCCGAGGGTTCATTTTCCTTTCGACAACGACGTTCAGT GGCGACCAGAGTTTCCCAATCACTTCAGCGATTCTATTCCTTCGTTGTAATAAAGCT TAAGGAATCCATGCTTTATTCCTTGGAAGGTTTGAATATTTATATTTGTTGGCATTAA TGCTATATACATCTATACTAATTTTGGGTTGTTCTAAACTTGTTTTGAATAACTTAAAT
SEQ ID NO:227	All	LPZ-195	GGTGCGATCCATGGCAAAGAGCTCGTTCAAGCACGATCATCCTCCAGAGAGAAGA CAAGCTGAAGCTTCTCGGATTCGAGAAAAGTATCCGGACAGGATTCCGGTTATTGT GGAGAAGGCTGAGAGAAGTGAGATACCTGATATTGATAAAAAGAAATATTTAGTCC CAGCAGATTTGACTGTTGGGCAATTTGTTTATGTTGTCCGAAAAAAAAAAAA
SEQ ID NO:228	Middle	LPZ-196	GGTGCGATCCCCTGTATTCTTGAAAGGGTTATAACGGAAGATAGCATTTTGCTCAG ATTGTAGACAGTCTGCATGATTTGTCAATACTACTATTTCGCATTATTTGTTAATACT ACTAATCCTTGTACTCATCTAGACTATTTAATTATTAAATTCTACAGTTTCTTTCTCCT AGATGGCAAACAATATGAATAAAATGCCAATAGTTTTGGAACTACTCCATTAAGAGC TTTAGATGATTATCATTCATCATTTGCCTGTTTTGAATCGTAAATGAATGTGTCACGG TCTTCTTTTCTGTTAGTCTCTATGCTTTCATCAGAAGAGTCTAAGCCAGTTACTGGA AGCTATTTGTCATCTCTTTAAACATTGTTTCCGTGCCAAAAAAAAAAAAAAAAAAAAA AA
SEQ ID NO:229	Late	LPZ-197	GGCAGAACTTCCAAAGTCTAGTATTTGATTAACTAATATGATGAAGACACTCAGTCT ATAACATGACGCCAGAAATCAGACCATATGCATGATAACTAGCACGATTAAAATACA ATTCGCAACCTTTAATACACTAAAAACGTTTACTGTATAGTCCACTCAGAACATTTC GATAGTATTGTCAGATCGACTTATTTAGCTCATATTCAGCAATCTGAACTGTACGAT GCGGCTCATTCAAGGGCATTTGGGTTTGCCCTTGGCATTCTTCATATCCCGATAGC AAGGACACGCGTTCTTGTTGCCATATGTCCCTGGGGGATCGCACC
SEQ ID NO:230	Early	LPZ-198	GGTGCGATCCAGATTGGCCAGGCCGGTATTCAGGTCGGCAATGCCTGTTGGGAGC TTTACTGTCTCGAGCACGACATTCAGCCTGATGGACAAATGCCAAGTGACAAGACC GTTGGCGGTGGAGATGATGCATTCAACACATTTTTCAGTGAGACAGGTGCCGGTAA GCATGTTCCTCGT181GCCGTGTTTCTGGATCTGGAGCCAACTGTCATTGATGAAGT TCGAACCGGCACATATCGGCAGCTTTTTCACCCAGAGCAGCTGATCAGTGGCAAA GAAGATGCCGCCAACAACTTTGCTCGTGGCCATTATACCATTGGTAAGGAAATTGT GGATCTGTGCTTGGATCGCACC
SEQ ID NO:231	Late	LPZ-199	GGTGCGATCCCAGCATTGGATGCATTTCTAGCACAAAGCCATCTTGACTAAAATAG CACTGCGGGCAACTGCAGTCCATAACTTTCAGAGCATTGTTGCTGCCTCAATTGTA TACCAATCCATATTCTAAAAATTAGACCTGGAAACCAGTCAGAAATTTAATGTTTTCT TGCAGAAAATGCCCTTTTAGAAAAAGGAGAGAATAACTGCATTCAAGTTCTAACTCC CAGACATAGCCTGGCAACGTCATTCATTCAGTTCGGATCGCACC
SEQ ID NO:232	E,L	LPZ-201	GGTGCGATCCAGAAAACAGCACAAGCAATCTGTAAGACCAATATTATTATCATCTCT CACTGCTCGTGAACAAAATGCTGGTTCATAGCCATCACGAAGGCTAAGGCTACTAT CCAGCCAAACTGATCTGCAACAATAATTTCATAAGCTTAAATAAATAGTCCATCCAG TGGATGGAGCCAGAAAGCCATAGAAACTTCAAATACTTGTGGTATCAATCTCTCCTC TGTTAAGGGAGGTATCAGATCAGAAGCACTAATCAAATGCATACATAAATGCAGTA GACTGCAATAAAACAAAATCTGCAGATAGCAACTGAGCGCTTAACGAACGGAAAAG AGTTTAACTTGATCTATCACAGGATCGCACC
SEQ ID NO:233	Late	LPZ-202	GAAAATGGGAGCCTCAAATATTCAAAGCCTCATCTCAAGAGTCTCAGATTCGGATT CATTTCATTTGGTTCGTAATAAAATAATGCATCAAATAGTTATTATCCACAAAAATGG GAGAATTATTACAATCTGTCTTCTCAACATAAAGTCATAGCATAGCATAGAACCACA CCACAGTCGTCATCATTTGTTTTGTTCACCACCGAAGGGGCTCTTTACAGCGTCCA TGAAGCCCTGTGTAGCACCCTTCGCCTTGTCCCCCGCCTGTTGGAAGAAAGAGCC AGTTTGTTCTTTCCCCTCTTGGGCTTTTCCCGTGATGGATCGCACC
SEQ ID NO:234	Late	LPZ-203	GGTGCGATCCTATTATAGAACCATGACTCTTGTCGATGGGGCATAAACTTCTCATTC TTAGGCGTGCCTACTGTGACTCTTGCCGATGTGGCATAAACTGCTTATTCTTAGTT GTGCCTTCTGTGCAGAACTTGTTGAGTCGGTGGATTACACTGAC
SEQ ID NO:235	Late	LPZ-204	GGTGCGATCCATTAACTAGATTAACGATAACATTCCTCTGCATCCAATCCAATGCTC ATCTAAATCTACTTCTACTTAGATCTCTGCCTCATCTTTCTCCACCTCCTCATCCATT CTGAAATATTAATTTCTGCATAGATTTTGTTAGGGTCTAGTAATCATTTTCATGAATT TAAATCTGTTCTAGTCTCTTATTATTATGCTGCTTATGCTAGCATCAGAACCTGTGTA TAATTCATTCATGTATATATTGGATTACACAAATTATACGGATGCCAGAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
SEQ ID NO:236	Late	LPZ-205	CTTGAAGCTGATATGTTTGAACCCGAAATTTTGTTACCCAACTCCAGTGTACATTGT GTCACTGTCAAAGAGAACATGAGAGCTGCATGCAAGCTTTTGCATGATAGATAGAT TACTGATCACCGAACATTTCTTACTCTACTTTCCTCTCCTATCCCCAGTGATTTTTG GGCATTTTCTATACCCTTCGGATCGCACC

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:237	Late	LPZ-206	CTCATGAACAGCAATATGATGCATTCCTCTTATACACATTTCATATATGTTCACCCTT GCCGTCATGGCTACTCTAAGAAGAGCAAAACAGACCCATTGAATCTTTACACGCGC TTGTTTATATGAATACAAATAATTTAGGCGTTTCTTTACACGCCCTTGTTTACATTAA TACAAGTGATTTAGGCGTTGTTACCAGAATAGTGCCACGGATCGCACC
SEQ ID NO:238	All	LPZ-207	GGTGCGATCCCAAGATAGAAAAGGGAACTATGGTCTCGAGGAGTGTCAGGTGCTA CAGATCACAATATACATAAGGGTCTGATAGTAGTACTCGGCCCAATGTTTGAGGGC TCTAACTAAGGAGGATCAACCGTACCCTTAGCCGTAAAACCCGACTACCCTATCGT ACGGGCGAGTAATCTCTCTGAGTGTTGTTCTCGGTGTATCGTAGCAGCAACACGG CTGACGGTTTATCTATGGTGAGGTTTCAAAGGAGCTAGGGGGCTTCCAATATACCC AGAGGGTACTTGGAAGACAGTTTATACGCGGTTCTGTCTAATGCGCTACTACTCGA AGGGGTACCCACAGGGGTTACAAGAGAGTGCAACAAGCATGACCACCCCTTGTAT TTCTTGCATGTATGCCTCCCCAAATCCGCAGGTTTATGCGCTCATTGACAGATTCC GTGGTTTAAAGATGCCGGAACATGTCTCTAGCCAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
SEQ ID NO:239	E,L	LPZ-208	GGTGCGATCCTCCTAACCTGCAATGTCCTTCCTGCAACCTGCAATTATTCAACAGA AATTAGGTT- TATTTTTCTTTTTGTCTTTTCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTTAAGTAAACGACCATTTCAAACGCCATTTCAAATGCTATGAATTAATGTT GAATTAATGTTAGCATTAAGTCTTAAACATTTTATGTTAAGGCATATATATCGTTCCA ACTACTCTTACAATACACCTGCGGTGTACTCCTGCCACCGCATGTACCACCGTTAC ATGTACGCCTGCCAGCACATCTAAGAGGTGCCAACTCCTTTGAACTCATCGTCGCC ATTTTTGTATGCATATTTGAACTCATCGTCGCCATTTTTGGTATCTTCACATATGGCC AGTGCAGGATCGCACC
SEQ ID NO:240	Late	LPZ-210	GGTGCGATCCAAGGAGTGGGCGTGCAATGCGTCGAAGATAGCCACCACTGCAGG GGCGTGGCATGCTGCCGTGCTTCCCACAGGGAGATCAACACCTGCACCTCCGCCT CCTTCCGCGGTTACCACGAG
SEQ ID NO:241	Middle	LPZ-211	GGTGCGATCCAGCCACAGAAAGATTGGTTTACTCGATAATTGAACGGTAGACTTTG TGCAGGTTTAGATTGTGTACATGCTGATCAGTATTGTCTACACCATTTTCAATCTTG TTTAGTTCTATGGTAATTTATGTAACAAATTCAGCGATGTTGGGGAAATTGGTCACA TCAGCTTTGTGCCTATATATTTCAAGTAAATCAGGGGATCCATTAATACTGCTTTTAA AATAATTGGGGCAAAGTTGTGGGATGACTGCTTCAGCGGAATACGTGCTTTTCATA GTGCTGTATGACATTTTGTTGAATATGAATTTTCTTTGTGATACAGTTGCGCGAAAA AAAAAAAA
SEQ ID NO:242	Middle	LPZ-212	GGTGCGATCCATGCCAAGAGGGTGACCATCATGCCCAAGGACATTCAGCTCGCTC GCCGCATCCGTGGAGAGAGGGCATAAACAGTCAGTCAGATCCAATGGTGTGTTTT CACACCACCATATGTTTCTTTTACTAAATTTGTTAGGTCCCTTCGGTGGGTCTTTTC TTTCGCCCGATTTTAGTATTTTGTTGTTCTTCTGAGTTTCATCATTGCAAGTACAAGA TGCAGAATTGATGGTTATTGGGACTTGGAGACTGGTTATTGCTATGTAGAGTATTTA TATTAGACAGGTTTCACTTGAAGATATAAAATTG
SEQ ID NO:243	Late	LPZ-213	GGTGCGATCCTCATGTGTTATAACCGAAGTTTGCGGGATTCAGATGGTCAGTATCT TAAATGTCCAACTTTCGGTACGAATGGGGTGCGTTCTGAAACGTGCCACGAAAGAG GTGTTCAGGATCTGTCTGAGGCATCTTTCCGGTATTTTCCACTTCCATGGTATGAG AAACTTTCGTCTTGTTGCAG
SEQ ID NO:244	Late	LPZ-214	AGGAGACACAACTTTACGAAAAAGTTCAATCTGGAGTCTTCTAAGTTTTTCAGACTC TCTAAATATGAAAAGCGCCGAGTTTCTCCTATACTGGACTCGTTAAAATTTTACAGT AAAGGACCTGTTCTATTACAAACAGGAACGGACCGCTCCTCCTTAGGGATCGCACC
SEQ ID NO:245	Late	LPZ-215	GGTGCGATCCAGCAAGAGAACGAAAAAGATATGAAGAATCTATGAAATATTTGTAC ATCACTGTATTCATATGAGGGCCTTTTTTTACAATGCGGTAGGGTTGTTTGGAGAAT TAGAACCTGATTAAAATGTAGATGGATTCAAGCTTTTAGTGAAATGAGGCT
SEQ ID NO:246	Late	LPZ-216	CTCAACATAAAGTCATAGCATAGCACCACACCACAGTCGTCATCATTTGTTTTGTTC ACCACCGAAGGGGCTCTTTACAGCGTCCTTGAAGCCCTGTATAGCACCCTTCGCCT TGTCCCCCGCCTGTTGGAAGAAAGAGCCAGTTTGTTCTTTCCCCTCTTGGGCTTTT CCCGTGATGGATCGCACC
SEQ ID NO:247	Middle	LPZ-217	GGTGCGATCCGATGGGATAGTTGCAAAACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTCGGGACCAAATATTTTTCAATACAACGCCATGTGACATTTTTGTGCTTCTTGT TTTTGATACATACATTCCAAAAACTGAACACTCGATGGATACGGTGATGATGCAGCT ACAGCCATTGCATTACAGATGTTATTAAATTAAATCAATTTATTATGTCATCACACCA ACCCAAACAATAGCGCTATTATGTCATTAGAATGGTTGCAGTTACAAGATCTGCAAA CAGATCAATGAATCATCATGCCCCTCTATATCTCTTGTCAAACATCAAGATAAACCT AATTTTAGGACTGGACTTCCTCAATCATATCACAATGGCAAACTCAGCCTCATGTCC
SEQ ID NO:248	Late	LPZ-219	GGTGCGATCCTGGACTGGCCATATGTGAAGATAACAAAAATGGCGACGATGAGTTC AAATATGCATAGAATAAGCGTTCTGTAATTGGAACGGCCATAGGAGTTGGCACCTG TTAGATGTGCTGGCAGGCGTACATGTAACGGTGGTACATGCGGTGGCAGGAGTAC ACCGCAGGTGTATTGTAAGAGTAGTTGGAACGATATATATGCCTTAACATAAAATGT TTAAGACTTAATGCTAACATTAATTCAACATTAATTCATAG
SEQ ID NO:249	E,L	LPZ-220	GGTGCGATCCCATGGGATAGTTGCAAAACACACAAATTTGTTGTGAAAGAAGAGAG ACACGCACAGACAACCATATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTTTTTTTTTTTGTGAAGTGACAAAATCTA AACCAAAGATTAAAAGGCTTTGGCTTCAGATACTATAGAAGAATGAGTCTCAAAGTG GACAGCATACTTGCGTTCCGAGCCTCATTTCACTAAAAGCTTGAATCCATCTACATT TTAATCAGGTTCTAATTCTCCAAACAACCCTACCGCATTGTAAAAAAAGGCCCTCAT ATGAATACAGTGATGTACAAATATTTCATAGATTCTCATATCTTTTTCGTTCTCTTGC TGGATCGCACC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:250	Late	LPZ-221	GGTGCGATCCCAACCAGGTGTCCATGCAATATATGGTGAGCATCAAGTTTGAGGTG GTTGATTGAAAGTTACAAATTGGTGACATCTGAAGTCTCATTCAGTTATGTTTTTGT TATAAAAACCATAACCAATTTTGTATATAAGATCCATAATCAATTTTGGCCAA
SEQ ID NO:251	Late	LPZ-222	GTTTTCAAGAAGAGCCTGACGGTTTCCTCGGCGGGATGACGGAAACAGGAAGCGG CCGGCCGGTTCCGGACCCTCCGCAGGCGGAGCATAGCATTTTGCCGGAACCACC GCATGTCCTGCACCCAACATCCGCGTCTGACCAGCGGAGGCACATGCACCCAACC CTCCCGGTTCCATTGCACCTCGGGCAGCGCGGCCACCCGCCGGGCATCGGCTTAT CCATCATGGATGGCACC
SEQ ID NO:252	Late	LPZ-223	TGGGCGAATCATATGGCTTGCATTTTCATTGTAACATGTATACGTTAAGGATTATCA TAATGCCTCCAAAACCTTGTATCTTCGTCCTTGCCACAATACATCCAGGATAACTAA TGGAAGCTTGACATGTCTTCACCAGTAATAATATATCAACTATAATACATGCCATTCT TTTATCAGTTTTGAACAAAATAATCGATTTGCATTCTTGACAAAGAACCTCGCGCAT AAAAACAAATAAATTCTCATAATGCCTCCCAAACCTTGTAGTCTGGGCCCTCAGTCG CCACAATCCATTTAAGAGGAATTTGGGGGTTGATAGTGCCCAGGTCCAATCTTCAT GAAAATTCGTTCATCAATCTTTGCTGCATACACATCTCTCTCTGCTTTCACTATCTG GGATCGCACC
SEQ ID NO:253	Late	LPZ-224	CCACTATAATGAACATTGATATTACAAATATAATATACATTAATATTACAATTCAAATC ATTGACAATGAGCAGGCACTACTTGCAGTGCTTTGGAATTCAGACTTCTGATTTGCA ATTAATTCTTGTAGACGCTTTTCTGGGAGGGCAGGTTTTCCGCTTCAGAGAAAACC ACGTACAAAACGATATTAAATAAAAATAGACACATACAAAAAATACTTCATTTTTTGC TCTTTCCATTTGGTTTCTTCCTCTATCTCCATTTTGGAGGGCTTAAATGACTTCAAAT TTAAAAGTCAACAACAGAGTGCAGCACATTCTATTAGCTTTGCTGTAAATATCTGAT TGGATCGCACC
SEQ ID NO:254	Middle	LPZ-225	GGTGCGATCCGCATTAAGAGAAGCATACAAGAAAAAGAAGTACCTGCCTCTTGATT TGCGTCCCAAGAAGACTCGTGCTATCAGGCGACGCCTTACCAAGCATCAGGCATC ATTGAAGACTGAGAGACAGAAAAAGAAAGAGATGTATTTTCCAATGAGAAAGTATG CAGCCAAGGTGTAAAGCACAGGATTTGAGCTTTCATGCAATTTTTTTGTTACTCGCG GGATGATATTGCCTATTATATTTCCGTCCAAGTTTTTGGCAAATTCCTATTTGCATCA GAATTCAAGTTATGATAGGTGTTCTTTCGTTTTTGAGCAGTTGATATTGTTTATCTTT TATTTCTATTATTAATCTTCTAAGTTGGATCGCAC
SEQ ID NO:255	Late	LPZ-226	AAACAGACAAATATAGAAATATGCATACATAAGTCCCTGCAGAATTGTTTTCCGCAA TGAATTCTGGTTTATGGCAACATTACCTACTTAGTACTAACCCTAAGATTATTTTCAG GTCTGATAAGTGGCATACGTGTATCAATCTTGCATGAGTCTATCCCTGTTTTAATCT TTTGTTGGGATCGCACC
SEQ ID NO:256	Late	LPZ-227	GTGGAAGCTTCATTGTAAAACACTACTGGTTTTGAGAGAACAAAATATATACGCTAG CCGAGTGGATTATAACAAAATATAGGCTTTATTCTATTGGATCGCACC
SEQ ID NO:257	Late	LPZ-228	GGTGCGATCCCATACATTAACATAGCCATCACAGCCCCCAGTGGCAAAAGTACCAT AGCTGCAAAAACATTATAAAACTAACATTCCTACAAGGAAATAAAATACAACTAAAAA AGCAAGCAATAGGCATTAGGGGAGGGAGAAGCTAAAACTATTAAGCAACTTACATG GGATGAAAGGCAATTGCGTTTACTGGATAAACAGTATCTCTGCCAGCCTCTGACTT GCGATGACATTTAAAGGCATATTTTTTAAGCTTGACCAGCTTCAGATACATCATAAT ACTCCATAGCCATGCGAGCTTCCACAGAACTAAGGGGCAAAACCTGTTCCATTTGG ATCGCATCA
SEQ ID NO:258	Late	LPZ-231	GGTGCGATCCAACTGAGAAGGGTGTTTGGTGGAAAGATGACACCAAGTGGGTTCT CTATTCTCCAGAGGATGCAAGAAAAATTCTGAGAGCAAAGAAGAATGGGGACTCAA ATATTACGTTGGGTTCTGTTAAATCTGCCAAGTACCCTTCAGGAAAGCTTTATGCCA TAGACCTGGTGGCCATGAAGCAAACCAATGTAAACACTGGCTTCTCCAGAGATATC AAAATCATCAATTCTTGCCCTACTGATGATCAGGAAGATGTAGAGTCTGATGAAGAA GATGAATTATTCACATTCTCTCGTCCTGTCAAAGTTGAAGTGATTAACCAGAGCAGG AAACCTGATAAGATTGTCAAGATGGTTCCTTCTGTCACTGTAGACCTTGAGAAATTG ACTTCTCAATACCTCCTGGAGGATGAGTGCAATTTGGTTCTAAAGCTTCCCAGGGC TGCAGCTGCCCAATCGGATCGCACC
SEQ ID NO:259	Middle	LPZ-233	GGTGCGATCCAGCTAATCAAACTTAATGGAGAGCCCTTCCCAGGAAGAGTAAATGG TAGTCACTTGAAGCCCTACACGGGTGGGCTGGCGGTCTGACTAACTGACCAAAAC ATAGTCTTCGCGACCCAACAAGCCAGACAGAGGTGTGGGACTATAAGCACAAGTAC TAGAAGCTAGCATCAAAGTAGAGAATTAAGTTAGATACAGATGATTCAGAAGCAGAA ATGGAGCAGATCCAGACCACGGTAGCATGGTGAGTTACGAACCTTCACGCCACAC CAACGCAATTGGTTAAGACTTCGCACTAGGATCGCACC
SEQ ID NO:260	Late	LPZ-234	GGTGCATCCATAGTTCCTTTTGCTAAGCGACTACTCTATCTCTTTTGACATTTCTCC AAATATTGGGTCTTTCAGTTCCTTCAAATGCTAGAATCATATCAACATGGGATTTAG TGAGGCCGCAATACTAACCAGGGCATTAAAATAATACATTTCATTGATCCTATTCCC AAAACATTTCCCGCTATCGTACGTTGACTCAGCATATTTAGAGCAATTCTTCTTACA AACCTTAAGAAGGTTGTTCATGATAGTCTTTCCGTCTGCAATATTGGATCGCACC
SEQ ID NO:261	Late	LPZ-235	GGTGCGATCCCACCCAAGAGTTAAATTCACTTCTCCGCCTTTCTGAGGAAGAGCAC TCTTTGGATGATATGAAAAGTGGTCCACTCTTAAAAACCGTATTCGGAACCCTGTTC CGCGGACGGTCGTATGGCGTAACCGGCGCAGACATTTTATCTCCTCACACAATATC AACATTCAAGTCCCCGCTGTTCCCCGTTGCCTTTCTCTGCTCCCGACCGTTAAACA AGAACGACCACAAGAATGAACAACACCGCAACCGAAACCTGACCCTGCACGTTGTC TTCGGTTCGGATCGCACC
SEQ ID NO:262	Late	LPZ-237	GCGGACGCCTGGCAAAAACAGAGGGTATGCTCAAGCCTTACAGAAATTGAAAAATA AGAGAACGTATGACCATCAATCTCAATCTCAAGAAAAGAAGTTGCAATACGACTCCA ACACTTTTGAAAGTTGGAGGTTTGCTCTTTCTAGCGTTGCAGACATGGTTGGTTTTG AGCTGGAAGCGTGTAACGGGCACTTTACAGTTGCGGGAATTGGAGATTGAGGACC CCCTCTCAAACGTCGATAGGGAGGCTAAGCATCTATAGAGGATTGTGATTGGTCCT TTTCCGCTACATGGAAAGAAAGTCAAACTCAGAAAATTACCAGAAGAATTCTGTCGT CTTCTCGCAGCCGT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:263	Late	LPZ-239	GACGTTGTAAAACGACGGCCAGTGTAAAGAGCAGCCCCGATGCGCCGAAGCTCGC GAGGGAAAAGCTGCAGAAGATGGGACCGATGACCAAGAATGAGATCATCATGAGC GGCACGCTACTGGTCACGGTGGGTCTTTGGATATTTGGGGGAATGCTGAACGTGG ATGCTGTTACTGCAGCGATCCTTGGTTTGTCTGTCCTACTCTGCACAGGCGTCCGC
SEQ ID NO:264	Late	LPZ-240	TACGGCTGCGAGAAGACGACAGAAGCAGAACCTGCCAATATAGGATCAATTGAATG TTGTGGGATTGCTGCATGCCCACCTTTCCCAGTTATTACTGCCTTGAAGAACCCAC AGCCAGCGAGTAAGGGCCCGGGTTTCGAACCAATCACAGATGTAGGATAATCGCT TGAAACATGCATAGCGAATATGCCTTCCACATTTTCCAGTGCTCCCTCGTCTATCAT TCTTTTTGATCCTGCACCTGATTCCTCTGCAGGCTGGAAGAGTAATATGACAGTTCC CTGTAACAAATGCTGACGTTGTTGCAAAATCTTTGCACCACCAAGAAGCATGGTAA CATGTGCATCATGTCCACAGGCGTCCGC
SEQ ID NO:265	Middle	LPZ-241	TACGGCTGCGAGAAGACGACAGAAAAGAGGCAAACCGAGCTCGACACCTCCACTC AGAGCATTTGCAAAAATCCACAACAAATCTGGAGCCAAGGTCTTTCCCTCATTGAAA ACATTTATCGGACACATCAATGTCTGTAGTCTTTCCCATGGTCCATCCAGAGTAATC ACGGGAAGAACAATGCACTTCAGTTCAGAATTTTTGATGACAGCTATCAGCTCCTG ATCCTTTGAACCAGGTATATAATAATCTTGACCTGACTCCTGTTTCAACAGTGTAGA GGTTCTGTCAACCTCAAGCAATGAATCGGCAGAACTTCCATTTGCTGTTTTGTCAAT ACAGGCATTGTTTTTACCAAGACTGTGACGCATCTTCTGTCCTTGTCTATACAGTGC AGTTTGTTCAAGCATAGACTTATGTGCTAGAACATGTCTTCCTTTTAAATTGTAAGA GAAATGTAGGGGTTGACTGCTTTTACTGAGGCGTCCGC
SEQ ID NO:266	Middle	LPZ-242	ACGGCTGCAGAAGACGACAGAACCCTGGCTGACTACAACATTCAAAAGGAGTCTAC CCTGCATCTGGTGCTCCGTCTAAGAGGAGGCATGCAGATTTTTGTTAAAACCCTTA CAGGCAAAACAATTACTCTGGAAGTGGAAAGCTCGGACACTATTGACAATGTAAAA GCTAAGATCCAGGACAAGGAGGGAATCCCACCTGACCAGGAGAGGTTGATCTTTG CCGGAAAGCAGCTAGAAGATGGTCGTACTCTGGCCGATTACAACATTCAGAAGGA GTCGACCCTTCACCTGGTGCTCCGTCTCCGTGGTGGCTTTTAGGTTGGCTGTTGT GTGTCAATGTAGTCTGGTGATGTTCAGTGGTTTTCCTGCTTAATCCTTTTTATGTAT GCATGTGTTTGTTGTGTTTGTGTTTTGTCTCTATGTTTTTTCTACTTGGTTTGTCGGT CGGTTGAAGCCCGGCTGGTGTCCTGGTAGGCGTCCGC
SEQ ID NO:267	Middle	LPZ-243	GCGGACGCCTGGACAAACACAGAAGGCGAAGTAAAAGCCAGTCTTACTTTTCATGT AAATACTATCAAACTGCATGGCCGTTCCGCTGGTTGGCAATACCACACCTGCGCCG GTAGTGCCAATGAACACTGCACCGGCAGCTCTTTCAGAAGTTGCAGAGGACTTACC ATTTTAATTTTCACGGCATCCCGTCAAACGGCGGGATGCTTTTAATTTTTTAATCAA AAAAAATATTAATTATGGCACACAATATTGTTTTCAACGAACAGACAGGCAAACACA GTTTCTTTAGTGTAAAAGAAAAAGCATGGCATGGTTTGGGGCAAATTGTACAGGAC TATCCCAACAGTAAAGAAGCATTGCAATTTGCAGGGCTTGATTTTGAAGTTTGCAAA AGGCCCAATATTCACAGGCTTGATAATGGTAATGAGATTATTTCTACCAGTTCATTC TATACTTAGCGTCCTGATACCAACGCCATATTAGGCGTCCGC
SEQ ID NO:268	Late	LPZ-244	GCGGACGCCTGAACATAGGAGCATTCTTAAGCATATCAGGTATAACCATAAACCTG ACTTTGCTGCCCCGAATAAAGACATGCTCCAATTGGGATACTTTTCCATCCTTGGCA GTGTAAGTGATGCCCTCGAGCTGGCAATTCCAGTTATCTTCGCATTCGATCATGCT ACCCCTGTACAGCTCGCCACTTTTGAGTTCAACTGTCACAACATGCCCGGCTGCTT CATGGAGCAACTTCACAGGAATCCCCAAACTTCTGCTCATTTTTTTGTCACTGCTCA AAAACCCTAAACCCCAGATAAAACCCTCGGTTCTGTGCCTTTTATCCCCGGGTGGC TTATTGTTGCAGTAGTTGGCAACGGCTAGACTTACTCACATTTTGATTTCAATCTTT CTAAGTTTGCCCTTTTGGGTTTTCCTCACAGTAGATCCTATTTTATGTATTTTCTCGT CTTCTCGGCAGCCGTA
SEQ ID NO:269	Late	LPZ-246	GCGGACGCCTGCAGGAATCGGCCGATTTGCAGTTCGAGGCATAAGCGCATCGAG GTCGCGTTCGATGTAGCAATTAAGCGCGCATGAACCGCCGCTAAGCAAGCCAGTC CCAATCAAAGCACATGCAAAGCGGATGCAATCAAATCTTCCGTTGTAAGCAAGCAC AAATCCAACTGCACATGAGATCACCACCATGAATGCAATTCGAGTGCGAGCTAAAT CCCAAAACGCTGCGAGTGTCCCCTGAAGGCGATTCGTATGTAATATTTGACCGCTG CTCAACACAAGCAGTACTCCAAACACCAGTGCTTCCGCCGTCAATTCTGTCGTCTT CTCGCAGCCGTA
SEQ ID NO:270	Late	LPZ-247	CTGCGAGAAGACGACAGAACACAGACACAAAATTTGGAAACTACAGAAAAGACCAT GTCATGAAATCTTCATAATTGGGCTTCAGATGCAGAGGGGGTCGGTTTTGGATTAA GCAATGGCTGAAGTGCTTTGACAACAATACTCATGTTAGGACGAAAATCTGCTTCAT ACTGCACACACAATGCCGCAACAGCAGCCATCTTTGCAACAGCCTTTGGAGGATAT TCACTCTTCAACTTGGGATCAACACACTGCTTTACTTTGTCTTCACTCAATCTTGGA GTTGCCCAAGTAACAAGGCTTTGTTGTCCCCTAGGCATTGTATGGTCCACAGGCGT CCGC
SEQ ID NO:271	Late	LPZ-248	TACGGCTGCGAGAAGACGACAGAAAGAGACAGGCTTGGACTTCGTGGCCTTCTTC CACCACGCATTATTTCTTTTCAGCAGCAATGTGATCGTTTCATGGTTTCTTTTAGAT CCCTGGAGCATAACACTCGAGATGGTTCAGCTGACTTAACAGCTCTGGCAAAATGG CGTATTCTTAACAGATTGCATGACAGAAATGAAACACTATACTACAAGGTTCTTATA GATCACATTGAAGAGTTTGCTCCAATAATCTACACTCCAACTGTAGGATTGGTTTGT CAGAATTATGGTGGGCTGTTCAGGCGTCCGC
SEQ ID NO:272	Early	LPZ-249	GCGGACGCCTCAATAGTTATGGAAGGGCAGCTGCACTACTTCAGCATGAGTGGAG GCCTAAAAGTTTTGTTAATCTTTCTGGTGAGGTGGACACCAAAGCCCTTCACAACA GTGCAAAGGTGGGGCTATCTCTGGTTTTGAAGCCTTGAAGGATATGCACTATTTGG TACAGATTTAAGCGAAGGTCTGTGCCAAATTTTTATTGGAATTTTTGAGTTTTTCCTT TCAGAATAATTATTTCAATGCCTGTGTTTTCTGTCGTCTTCTCGCAGCCGTA

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:273	Late	LPZ-250	GCGGACGCCTTTTGCCCAATTAACATCCCTGCATCTGCGCATTAAAAATTGATTGC AGACCTGAGGTTTAAGTGGAAGCTTCTTCCACCATCTCTCCCCTGTTTAAGGAAGA CCCGAAACCCTAGCCACTGTCTCCTCTGTGACTTAAAATTCCAGTTCACCAACCTTA ACTCTGCGTCCGTTAAAATTCTGGGCAAACTGCACTGCCAATTGGTCATCATATCCT CTGAATTTGGCAAAGAAAACATAGGTCATTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:274	ND	LPZ-251	GCGGACGCCTCGTCAATCCATGGTTGTAAACATGCCTTCAAAACTGTTTCCTTATGT CGCACAATGTCTACATGTTCCTTGAGCGATTTTTCCTGCTGCATTGCGAGCCTCTG TGTAAGTCCCACTATCTGCGCTGTCCCTTTTACTTCATAATACTTCTGTCGTCTTCT CGCAGCCGTA
SEQ ID NO:275	Late	LPZ-255	TACGGCTGCGAGAAGACGACAGAAAAAACTGTATACGAGTAGGCAGCGAGTCCTG GCAGTATGGGAGATTGAACTCCAATTACATTTAGTTACAAGTAGCATCAACAGTGAC TGAGCCAAGAGCTCTACACAGAAAAATAAAATAAAAACTGTATATATTTACAGGAGA AACCCCAATGGCCTCAGGGCCTGAATAAATCAATCGCAGCGGTGGTCGATGTGGC CTTTTCAGGGCTGCAAATCTTGCAAGGGGAAGCCATCATCCTTGTTCCGTATCCTT TTTGAGGGATAGCGAGCCACGCAGCCAAGATTTGAAGCGATTGAATACTTTGGGGT GTCGAGAACGCACCAGAACAATGCCACTCGAGAAATACTACTGTGATTACTGTGAC AAACAATTCCAGGATACTCCCTCCGCTAGAAAGCGACATCTACAAGGCGTCCGC
SEQ ID NO:276	Late	LPZ-256	GCGGACGCCTGTACCGTATTGGAATTCTAAACCCTTCCTTGGTATAGGGTTTTCGC CACCCTTGCGTTCATTTGGTTTTGTATTACGTCCGATTCCTCCGTCTGCGAGCTCTC TGCAACTTGGCAATTTCATTGTGATTTTATCCTATGATGCTTCGTATTTGTTTGAAGC TCGTCCTCCTAGTTCTCTGTGATACCAGTTGGTAGTCTGCAAGTTTCGATGTGGGT TCTTTTAGCTGGTCTGGGGTTTTGTTGCTCTGAGTATGTTGAGCTGCATGCTCGTG GCGGTCTTCACGGCTCCATTTGTTCGGAATCTGTTGTGGAAGTGTCTCGGTCATCT GTGGAACTGTGGAAACCTGGTAAGATTTGTTTATCTGCTTGTGTCTAAACTGTTCTT GAGTTTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:277	Late	LPZ-257	GCGGACGCCTGCTGTTGAAGAAGGATGAAGTCATTGTCTGCGGCCCTGTTCAGCA TGATTTCGGCATTCTTAATCTGGTCAACCAGTCAGAAGGTGGCGCTGAAGGTGACG AAGAGGCAACCTGGGTAGCTGCACTGGAAACTCAAGCTGCAAGGGGCACCGACCC TCAGACTTCGCGCGATTAACTTCTCCCTCTGGCTAAGTCGATGCCAAGGTCCTTGT TCTGGGTTCTTCTCTCTGTTTCGCATGTTGTTCTTCTCTCTGTTTCATTTGTTTTTCT TCTGTCGTCTCTCGC
SEQ ID NO:278	Late	LPZ-258	GCGGACGCCTGCACATACAAAGAACGACAAAAACAAAAGCATAAAATCCAATAGAT GCAACTATATATCAAGTCAGAAATGATATAACTCATCATTATTACAAAGAACAATAAG AGTGGAACCATAATAATAGTCGTCTATTATTGATAAATAAAGAAGAATACAACCATA GTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:279	Late	LPZ-260	GCGGACGCCTGTATAACATGCACCAAGAGACCCAATCAAAGCACATGCAATCTGTA TATATAGCAGAATAACAGCCAGGGATTGCACTCTATCGTAATCGCGAAACCACGCA CTAATATGTGCCCATGCTGATGATGCACACAGCATGTTCTGTCGTCTTCTCGCAGC CGTA
SEQ ID NO:280	Late	LPZ-261	GCGGACGCCTGAACTGTATAGAGTTGAAACTTGAGGGAAGGCTTGCTGCCACCAA AGCCTCCCTCCTCTTTCCTTGGCGGTTCGTCACCTCCTTTCGCGTCAGAGCCCCAA TTCCCCTCCTGCGCACACCAGCAAACTGCATCGAATGTTTTTTCCACCATTCTGTAA ATTCCCTCGGAGTTACCTTGGGGCAGAAGCCGCATTGAAGAGCATTGAATGCTATT CATTATCCCACCGTAAACTACCATTGCAACCTGCCTGTGTATCGACCCGCTGTCCT CTACGCGTGGCTGGCACATGGCGTCGTTAATTGCATGTTGACACCCGTATCCGGG TGTGCTTGTGTGCTCGTCTGCATATCATGTTTTAGGATCTCATAGAAGGTGGACCA TTCTGTCGTCTTCT
SEQ ID NO:281	Late	LPZ-264	GCGGACGCCTCTTACAATGTCTCTTAAAGATTGGAAAGATTGTCTTGTCTGCAACC ATAACTTCCGCGTGCTTTCTTATTAATGCAACCCACTGTGATCCTTTCCGCCATTTA TCCTTTCGAATGGTTGGAGCCATTTTTGGGTTGTACCGACTAGCTTTTGGGTCTAC AAAGCTGTCTACAAAACTCTTTGGAGATGACATTACATAATCATATGTATAGCTGAA GTTGTACAAAGGTACACAACTATCTGAAACCAAAATGAATCTCTCGTTAGCTGGATC CTCGAGTGCTTTCCTAAGTAGAATACGCTCCGCTTCTATCATACTGGCTTCTCCCCA AAGTACCTGTATGCTATCACTAAGCTGCCAGCCGTAACAAAATGTACATTCTGTCGT CTTCTCGCAGCCGTA
SEQ ID NO:282	E,M	LPZ-265	GCGGACGCCTTGCTAGGAGAGCTCTACGCCATTATTTGAACGATTGAGCCGAAGTT TCACCGTTTAAGGCATTTGTGTCCCAGAGGTTATTGGAGATTAGCAGCTTGGATTT GGCTGCTTCGCTCAGCGCCGTGATTCAGCTTTTGATTGATTCTCTCCAGTTTCATAA CCTGTAACGACAATGGCAATGAAGACCTACACATTTGCAGTGGCAGCTGCGTACGC TGTAGTCCTGATGTTCGCTCTCTTTGGCATCGCAAAGGCTGCTGATGCACCGTCTC CCAGCCCCGTTACTGGCGCGGGTTCCATGGACTTCGTTCCTTCTGTCGTCTTCTCG CAGCGGTA
SEQ ID NO:283	Middle	LPZ-266	GCGGACGCCTTATCAGCTGGGGGCATTCATAGGTATGGAAATTCAGATCAACTTCA GTGGACAGTATGTGGATTTAGGCGACCTGTGACAGTTCACGATATCTATTCATTTCT ATCCAGAGACAGATTCCCATACTCACCTCCGTCCTTCCCATATATTTTCTGGAAGGC ATCATGTCCTCCCAAATTTACTCATTTTGCCTGGCCGTCGTTTTACAA
SEQ ID NO:284	Late	LPZ-268	GCGGACGCCTGTTGCCACAGAAGAATGAATAATGCTTCAAATTTTGAGACCTCTTC GGAGGAAAATCCTTGTTCTTACTGCCTAACCACTCATGATGATCTGCGTCACGCTG ATTATGAGCTGCAATTTAAATTATTTCAGATGAAACATTCCCATATTGAGCTTGCAGA CAAGTTGCAGACCCTTCAATTTCAGTTCTGTCGTCTTCTCGCAGCCGTA
SEQ ID NO:285	Middle	LPZ-269	GACGTTGTAAAACGACGGCCAGGATTAAGGTTCATGAGCTCCGCAACAAGAGC TCAG
SEQ ID NO:286	Late	LPZ-270	GCGGACGCCTCTAGGAGCCGGCGGAATTCCTGTGAGCTCGAATTTGCCGAGCAG GTTATTGTCCTTCGTCCGCGCTCGCTCACCTTCATATACTTGAATTAGAACCCCAG GCTGATTATCTGAGTAAGTTGAGAAAATCTGCTCCTTCTTGGTTGGAATGGTGGTG TTCCTCGGTATTAATACTGTCATTACACCTCCCGCTGTCTCCAACCCCAGACTTAAT

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cDNA	Embryo Phase	Clone	Nucleotide Sequence
			GGCGTGACATCTAGCAACAGCAGGTCCTGCACCTTCTCGTTGCCTTCGCCGCTGA
			GAATGGCAGCCTGCACAGCTGCACCATATGCCACGGCTTCGTCTGGGTTAATGCT
			CTTACAAAGCTCTTTGCCATTGAAGAAATCTTGGAGCAATTGTTGTACTTTGGGGAT
			ACGAGTCGAACCCCCGACCAAGACGACATCATCTATTTGGCTCTTGTCCATCTTAG
			CATGTTCGCATACATTTCTCGACAGGCTCCATACTTCTCCTGAAAAGATCCATGTTG
			AGTTCCTCGAAGCGAGCTCGCGTAATTGTGGCGTAAAAATCAATTCCTTCATATAG
			AGAATCAATCTCAATCGTTGTCTGTGTAGTAGAAGACAGCGTTCTTTTTGCCCTCTC
			ACATGCTGTTCTCAGCCTGCGAAGAGCTCTGGCATTCCCGCTGATGTCTTTTCTGT
			GCTTTCTTTTGAATTCCTGCACAAAGTGATTCACCATTCTGTCGTCTTCTCGCAGCC
			GTA
SEQ ID NO:287	Late	LPZ-271	TAGCCATCGCCATTTCTATAATCTTAGGATCCTTGCTGAACGATAAGCCCATAAAAT
			TGATGCACTGCCTCGCTATCCCTGGCCGTCGTTTTACAACGTC
SEQ ID NO:288	Middle	LPZ-272	GACGTTGTAAAACGACGGCCAGGAAATTACAGCTACCTCTAACTGGTTTGACGGCG
			TTGCATCTTATGAGCCGCAAGGGTTCGAATCCTCTGCGGGCCAGATCTGCGATGG
			AACCCTGGGCGAGTGCAATGATGATGAAGAAGAGTTTGCGATGGATTCTGAAGCG
			CACGGGAGGCTTCTGAGGAGGATCCGTTACTATATCAGCTACGGAGCATTGGCTG
			CTAATCGCGTTCCTTGCCGACCTCGGTCTGGGAGGTCTTATTACACTCGGAATTGT
			TACGGCGCAACAGGCCCCGTCAGACCTTACCACAGAAGCTGCACTGCTATCACTC
			GTTGCAGGCGTCCGC
SEQ ID NO:289	Middle	LPZ-273	GCGGACGCCTGGGAAGCAATGGATGGGTGGCTAGACGCCATCCGTCTTGTGTATA
			CTATTTTTGCACGCGGAAAGAGTGATGTCCTGGCCGTCGTTTTACAACGTC
SEQ ID NO:290	Late	LPZ-274	GACGTTGTAAAACGACGGCCAGATTCAAAAGAAAAAATCCTCACTTCTTGGCTCCG
			TTTGCGGTCCCGCCGAAGCTCCTCTGCAACCCCTCTGCAGCGTACACTGCATCCC
			GCTCGCGGTGCTGGCTCACCTCGCAGGTCCGCTGACGGTAAATGGTTTCCAATAA
			AGCTATTTGTCCTCTACCCAAAATCCATCTAGCATTCGTTGTGGATTGACATTCTGC
			CATTTCTCTGCTTTTCTGGTTGATATGCAAAGATTGAAAGCCCAATTGCAAGCAGTG
			GTCGTGGATTCACTATAAGGCGTCCGC
SEQ ID NO:291	Late	LPZ-275	GACGTTGTAAAACGACGGCCAGGAATAAAACAAAGCATCACTGCAAAATTTCAAAC
			GTGGTAATAACGGCTAGCGAGCTCGACGTGAAGGCAGTGGGGGCCTTGAGGTTGC
			CTTTTGGCGTTCAAAATTGGCTAGACTACCATAACATAAATATTGATTTCTCAGTGA
			CATCACTGGTTTGGAGTCATCCACAGCCTGTGCACCAGTACGGCAATTGCCTTTTA
			CATGAAGCCATCCTTTCACTTTTACTTTTGAGATTCTCAGAACTGAGGGGCTAGGC
			GTCCGC
SEQ ID NO:292	Middle	LPZ-276	GACGTTGTAAAACGACGGCCAGCACCTTCCTAGTCCCCTGTTCCATTCTCCTGAAA
			TAGGAGCAGTTTGACCCAGTCCAGTTTTCAGAATTGAGAATATGAAACAAAGAACCT
			AAGCATATGAGAGAACATACAAAGACTTTGTATAAACTACTTTTCACAGGATCTCAA
			CAGCCCTCTGCTGAGATCCATTTGATACAAGGCCCCTTGCATCTCCACCCTCTCCC
			TTATCACCTCCACTAGAAAGATGATGGAAAGCAGACACATGGAAATGTTGCTGCAG
			GCGTCCGC
SEQ ID NO:293	Middle	LPZ-277	GACGTTGTAAAACGACGGCCAGTTAGGTTGTATATTGATTGATGACTCTTTGACTCC
			ATTTATGAAAACATCTTTGTTCTCGAGATTTAATCAGTATTAAGCTTTCAGAGTGAAG
			TTCAGTTTGATCTGCATAAACCTGATCCACCATATCTACATCACATCTAAAATTACTA
			AAATGTGAGGAGATGGAATTTGTTTCTTGAGAATCCCTATTCCTCATCGACACTGTT
			TACTGGATCAGATCCAATCAAACTCTTGAGAAGTAATCTCTGGAAAGAAATTAAAAA
			GTCTTTACCTGAATTATCTCGATATCAGAAGCAGAAATTATGATACATAGACTTCTTA
			ATAATGAAGAGTCATTTTGCCAACGTTGTCTTTGCCACCCCACCAATCCCCATGATC
			CCAAAGATCTGAGGTTTCCATCTCTATGTGGCTGTGATAACACTGGATTTTTCAAAA
			ATCTTCTACTTTCGCATCCAAACCTTTTTGGGATATTT
SEQ ID NO:294	Late	LPZ-278	GACGTTGTAAAACGACGGCCAGGGGGATGGGAGATACAGAAAGATTCCGGATAAA
			AGGGAGCAATGAACGGCTGGTTAAAGCGTAGTCCACCACACTAGCCCCACCTCCA
			TGAGGCCTACACGTGAAGAAGCAGGATTCTGGGAAGCGCGAGAGGCCGTTCAAGA
			TTATCAGCTCATGTGATTCGCCCAACTGCAAAAGATGTCTACCGTAGGCTGTGATG
			GGGCCCAAGGCGTCCGC
SEQ ID NO:295	Late	LPZ-279	GCGGACGCCTATCAGATGGGTGAGTTGACCGACATTTATCGTCCGATAAATGTTTG
			AGGCTGATGTCATGGCAATCCACGTGTCTGCACCATATTTCATCGGAGCCCCTCGT
			CGGAATATTCCATCGCCGGAGAGCTGGCGCGATAGGTTTCAGGCGGCCGGTTTCT
			GGTTTGCAGCTGTGGCTTCCCGCGCGCCTTAACTGTTGGCCCGCGCGCACAGGG
			GAAATTACAAATTTCAACATATCCAATACCATCATATAACCCAACAACACTAGCAACA
			GATCCTGTTCTGTGCCATCGTCCAACTCTTGA
SEQ ID NO:296	Late	LPZ-280	GCGGACGCCTTAATTCGACTACAAAGATACTGAAGCCAATGATGACAGGTTGTGCC
			ACTTTCCCAGCTGATAAAGACAGCTCTGAAATTGATAGAGCCAGAACTCCAGCTGC
			AATGCTCCCCAGAGCCTGGTTGAAGCGCTTGCTAAAGGTGGCACTTTATAGACCGA
			CCCAAAACCTCCCTGGCCGTCGTTTTACAACGTC
SEQ ID NO:297	Early	LPZ-281	GCGGACGCCTACTGGAAACCCGGTCCACCGAAGGCTGAAATTGTCCTGCTTTGTA
			TACCGAATGGCAGGAAGGTTGTCGAGCATCAGGTTCACCTGGTAAAGATTATCGAT
			CCTATGCTTCAATACCTTCAGCTGCTCTGCCCCAAGGACAGTAGTATTGCACAGGT
			AAATTTCAGATTCATTGACATTCATCCGGAAGCGATATGGTGAGTTCTCGATCCTGT
			CCCCCATGAGGAGCTCCCCAAGATTTTCTGCCATGTCCTTCACACCATCCAAGGGC
			TTGCAGAAGGGCAGGCTGTAATAGCTGTAGGGAAGCTCTGTCTCGACTGAGGTAA
			GGGAATTGACGTTCACCCATAAATCTGACCCCTGGGAGAATATGATGTGAGGAATA
			CAGTGCCCAGTAAATATAACTCCGCATTATACGTTTGTGTGTGCCTTCCCCAATATT
			GCCCCAACATAATCAAAACCCACAATCCCAAATCCTGGACCGTCGTTTTTACAACTG
			TC
SEQ ID NO:298	Early	LPZ-282	GCGGACGCCTTGTCAGGACCAAATGTGTAAGAAACACCTCTGTCATTCGAGCCCCA
			TCCTTGAATTGCATTGCAGGGGTCTGACCAAAGAAGATCACATAACAACCCTGTAT
			CTGGCACATCTGTAGGTCGAGGTATATTCTTTATTTGTTCCAAATTGGTCAGTTCAG

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			GCGAAAGACCACCATGCATGCATAGGATCTTTTCATCTATAAGTGCAGCAACAGGC
			AGGCAGTTGAAACAGTCTGTAAAAAGTTTCCATAGTCTTACATTGAATCTGCGCTTG
			CACTCATCATAGAAACCATATATGCGATTTATTGAGGCACATTCATGATTTCCCCTC
			AGAAGGAAAAAGTTCTCTGGGTATTTAATTTTGTAAGCAAGGAGGAGGCATATTGT
			CTCTAGGCTTTGTTTGCCCCGGTCCACATAATCTCCCAAGAAATAAGTAATTTGATT
			CTGGTGGGAAGCCACCATATTCAAAAAGCCTTAGACAGATCAGAATACCGGCCTGT
			CGTTTTACAACGTC
SEQ ID NO:299	Early	LPZ-283	GACGTTGTAAAACGACGGCCAGGAGACGGGAATACCTATTTTTGGGAGGATTATTG
			GGCTCGGGAATCAGCATATTGATGTGGCTGCAACTCGCATCCTCGATCTTTGGTGG
			TTCTTCGGCGATTTACACATTTGAGATCTACTTCGGTCTGCTAGTTTTCCTTGGGTA
			TATTATATTTGACACACAGATGATCATCGAGAAAGCGGACCATGGAGACTATGATTA
			TTTAAAACATTCACTGGACCTCTTTATTGACTTCGTTGCTGTATTTGTTCGCCTGAT
			GGTCATAATGGCAAAGAATGCAGACAGTAAATCCAGGGAAGGGAAAAAGAAGAGA
			AGGGCTTGAACTATGTGAGATACAAAAATATCGAGAATAGAAGGGCTTGAACTAGG
			GCTTGAAAGCGTCCGC
SEQ ID NO:300	Middle	LPZ-284	GCGGACGCCTATCAGACAAGGGTTGTTGACCGAACTTTATCGTCTGAAAAGTGCTT
			GAAGCTGATGTCATGGCAATCCACGTGTCTGCACCATATTTCATCGGAGCCCCTCA
			CACGGAAACAACCTTAAGCCAAAAGGTGGTGCGATGACTTACCGGCCGTTTATGGT
			TTGCTTCGGTGGTTTTCTGTTGGGTGGTTTCCCGCGCGCGTTAACTGCTGGCCGT
			CGTTTTACAACGTC
SEQ ID NO:301	Late	LPZ-286	GACGTTGTAAAACGACGGCCAAGAGGGGGAAACTCCCAAAACACTTTTCCATTTTT
			CTTCTTTTATTAAACTTCAAAGTATTTTCCAACAGAGTTACAAGGGGCCAACCATGT
			CCAAATCCATGCATTTACCAAGTACAAAGAATGGTAGTCCTTGGCTTGACCTATCGC
			ACTAGCCAAAAGTGCCAAGTCCACAACTAGGGTGTGCCCAACCTAAGGTTGACACC
			TTGCCTAGAAAAAACCCCAAACTTGGCACCACAAATAACACAGAAACACAACTCTTG
			ACCTCTGCCAGAAACCAGGCTCTCTTGGGAAAGCCACACCTCTCTCTGTGATATGT
			CTTATCTCCAATTTCCCTTTTTGTGATGCACTCCCTTGCTTGTGGTTCTGCGATATC
			ACACAAACTTACATTTCTGCGATTTTTGTTTCTTGCTTCTCCAAATCATGCGATCTTA
			TTTTTAACCCTTGAGACCCTTCACACTTTCCATCCATGACGTCACTTCATCGTTTTA
			GCCAATTCGTCATTTGGGCATGTTGGGCGTTGGGTCTACCCGTATTCCGGTCGTAC
			AGGCCAAATTGAGCATTTTGGTCCAGGTGGGTGCACCCATTCCTGGAGGGCGTTC
			GGC
SEQ ID NO:302	Late	LPZ-287	GCGGACGCCTCCACAGAGCTCACACATACAATATACTATGATGCCTCCAGAACTAT
			GGCACTCTGTATGCCGCTTCAATATGGATTAGCCCACACTGCGCCATCCAATTAGG
			CGAATCAACCTTATAGCACCATCCACAACCTCCAGCGCTCTCTTTTTCACGCTAGAT
			TGGCCAACTACAGGGTTTACAACACTACTCATATACAACTCAACTCGGCTCCTCTGC
			TCACCACTAAATGACACAGGCTCCAATCGCTAGACAGAGCCACTACACAGGCAGTA
			ATAGCCACTACACAGGCACTAATCTTGGCGTCCTCCACCAGGTTCCAACAACAACC
			CCAAATTGCATATGCACTCCACAGTGAGCACCAACTAGGTCCACACAATAGGCCAC
			ACCAACAACACTCCAAGGACCCTAGATCCTGCCTCACCCAGACACCACTAGGCCTT
			CCTCACAGCTCACCTAAGTGAGCCAACAACTGGCTGGGCACACAGCTCCCAACTAT
			ATGAGCACACAGCCCAACTACAGCTCCACCACACGCACAGCTACACGCACAATGC
			CTTCTCAAGTTCACAGCCACACCATAACGCAGCACAGTTCTTACAAACATATCTCTC
			CAGGCGTCCGC
SEQ ID NO:303	Middle	LPZ-288	GACGTTGTAAAACGACGGCCAGGATAATGGACACGAGAAACCTTTGGATGTGCCT
			GTAAAGTGCGGGCAATCCTTAAAGCTGTTGAATTTTGTTGCTGTACACGAAGGTGC
			AGGGTCTTTATGCCACGAAGAATCAAGTACGCTGCATTTGGACTTAATACACCTCC
			CAAGACATTGTGCAAAGCACGTACTGTGCCAATAACCTTGTTTGAACCACTCAAACT
			GCCTGCAAGAACATCATTATGACCTGCAATATATTTAGTTACCGAATGCAATACAAT
			ATCTGCGCCGAGTGCTAACGCTTTCTGGTTAACAGGCGTCCGC
SEQ ID NO:304	Middle	LPZ-289	GACGTTGTAAAACGACGGCCAGTCATTATTGACAATAATCCTTTCAGCTTTTTACTG
			CAACCTTTAAACGGTATACCTTGCGTTTCTTTCACTGGAGCACACTCAGATGATAAT
			CAGCTTTTACAGGTGCTCTTACCTCTGTTGAAGCATCTTGCCACTCAGGAGGACGT
			GCGCCCTGTGTTGTATGAAAGATTTTACATGCCCGCATGGTTTGAAAAGCGTGGCA
			TTCCAGCATCTGAGTGGCCCTTGTGACTTGGTTTTGATTTTGGATACTCTTTGTCAT
			TTTGGGTCAAGGTAAAGGTGTACGTATCCAAGTGATGCAAGCGTCCGC
SEQ ID NO:305	Middle	LPZ-290	GCGGACGCCTGATAGCACGAGTCTTCTTGGGACGCAAATCAAGAGGCAGGTACTT
			CTTTTTCTTGTATGCTTCTCTTAATGCGGATCGCTGGCTCTGAGAAATCACAGTCAG
			AACCTGAGCTATTGATAGCCTCACGACCTTGATTTTAGAGAGTTTGTTGGGCGCTC
			CTCCAGTGACCTTTGCAACTCTGAGCAAGGCAAGCTCAGCCTTGAGCTCCTTGACC
			TGGCTTAACAGCTCGGATTTGCCCTTGTGGCGGACTCAAGGACCTTTAACCTGGG
			CGTTCGT
SEQ ID NO:306	Late	LPZ-293	GCGGACGCCTGGTGTCGCTGGGCCAGTTCAAGTATTTTAGCAACAGTGTTCACACT
			TATTCCCTGTGATATTCTTGACTCACACAACCACCTTAACTGACGCAGACCATATCG
			ATCTGCTGCTGTAAGCAAATGTTCGATCATTGTCTCAGGTGTCAAAAAGCAAGGGG
			ATGGATCAGAAAGCTCTTCTAAATCTGCATGCTCCTCTAAATCTGGAAGGGTATCTT
			TGTAAATAAAGTGTAACATAGCCTTAAACACCTCTGGCCGTCGTT
SEQ ID NO:307	Late	LPZ-294	GACGTTGTAAAACGACGGCCAGAGGTGTTTAAGGCTATGTTACACTTTATTTACAAA
			GATACCCTTCCAGATTTAAAGGAGCATGCAAATTTAAGAAAAACTTTCCTGATTCAA
			CCCCCTGCCTTTTGGCACCCTGAAGATGGTTCAACAATTTGCTAACGGAACCAATT
			CAAAAGGGCCGCCTCCATTTAAGGTGTTGTGTTAGTCCAGAATATCACAAGGAATA
			AGTGTTAACACCGGTGCCAAAATACCTGAACTGGACCAACGACACCAAGCGTTCGC
			C
SEQ ID NO:308	Middle	LPZ-295	GCGGACGCCTTGTAATCCAGGGCCTTGAATATTGTAAGAGAAGATCGAGAAATAAT
			AGTTTTCTTATTATCAGGAATCACAGCTTGAAGAAGGCAGACCATGGACTCCCACT
			GGCTTCGTGATATTGAGTCCCCAACAAACATTAGTCGTTTTCCCCTCAATCTCCACA

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			GCAAGTCTCTGGCATTGAATCTGCGAAAGGAACACCCGAGTGGCTTCCACCTCCAT
			TTCTCGTAATCAGAATCTGGCCGTCGTTTAACAA
SEQ ID NO:309	Late	LPZ-297	GACGTTGTAAAACGACGGCCAGCAGAAGACCAGTGCAGTATGCTGCAGCATAGTT
			TGTAAGCCCTACTTCGAGTCCATAACGAGGCAACTCCCTAGAATAAGCAGCCGACA
			TAACAACATCTCCCGCAAGAGTTGCATAAATGATCTGTGCCACCACATCCTTGTTGC
			TGAATCTAACGACCAATCGGTATTTGGGTGTGTTGTACTTGTTCTTATCTTGGTTAA
			TCAGGCGTCCGC
SEQ ID NO:310	Late	LPZ-299	GACGTTGTAAAACGACGGCCAGCATCCATTGCAGAAATTTTGGGGGCTATATTTAG
			CAACAGATATCACAGCTGTAAGTTCAAAGTTGGACCCTTCTTCTTCGACATCTTTTC
			CAGCTGTGCAATAAACTGAACACTGTCCTTTTGGATAAGCTTCCTCAACATATTTAG
			AAAGTTCAACATCCAAGACATTGCGGTACTCCTCAACATATATGGATGCAAGTTCAT
			CATCTGCAGCTGGTCTCACCGCTGTACAAACTTGTTTAACATGGTTGACAGTTGCA
			ACTTGAGCAGTCCGTGGATCCAAATAATGAGTTCCGTCAAGCTCACTGAACTCAGT
			CACAATCACCTGGCCACTTTGATTGGGCATCTCGAGGGATATCATGTGAGACTTGT
			TGTGGATGGGGAAAGCGTCCGC
SEQ ID NO:311	Early	LPZ-300	GCGGACGCCTGCATAAACATCGCTACCCTGGGGATGATTAATAATAGTACCAGGGT
			TAGGATTTTCTTCATCTTGAGCGATATCATCATACATAAAGACCACAATGTTTTCCTC
			TTTCAAACCGCCTTTCCTCAGAATTTGGTAGGCATGGCAGATATCAGCCTGATGCC
			TGTAGTTCCAATAACCGGAAGAACCAGCCAACAGAATAGCCCACTGAGTACCGATC
			GTATCACTATCATCAACGATATGATCGGTGGGCATTTTCAGTACTGAATCCCAACCC
			CTTCTGGCCGTCGTTTTACAACGTC
SEQ ID NO:312	Middle	LPZ-301	GCGGACGCCTAGACTGGGCATACCAACTACCTTCCTCATGCCAGGCCATGGGCCA
			CCTACCTGGTACTTAGGCATAACACCTTACTTACGAGCATGCCAGGCTCAGTCAGA
			TAGGCATGCATCCCACCCACCTAGCTATGACCCAATCCTTATAAACACTAGATATTC
			TCCCTGGCCGTCGTT
SEQ ID NO:313	Late	LPZ-303	GCGGACGCCTAGACAATCATTAACTGAAGATCTGTAAGCCATGACAAGACGAATAA
			AACGAAGCAGGGCGCAACCAGCGTGAATATTGACGCCTTAATTTCATTCAACTGGG
			TTGCGGATTCTTTATTCCTCAACAAGTGTTCGATAGCTTCACATACGCAAGGCCCCT
			TTTACTCTCACCTTCATGGTTTAATGCTGTAACCGTCGAAGGTTGATGAAAGGACTT
			GGATGATGATGTTGCCAAAAAAAAAAAAA
SEQ ID NO:314	Middle	LPZ-304	GCGGACGCCTGCTCAACACCTGTTATAGTCATTTCTTGTTTCCTTTTCTCAATTTTC
			TCTTTCGAATGACCGCATTGAAATTCAGGCTGCCCAACGCGTTTTTGTTTTCACAAT
			TAATTTTTGAATCATACGCGAAGATCATGATGAGAATGGTTGTGGAAAAAAACTGTT
			TGTAAATATTTAG
SEQ ID NO:315	Middle	LPZ-306	ATATCACATTACCATTCAAAAAATAAACATTTTACAAAATACAATTCCATAACAATTTT
			CTTCCCTGTTCCAACCTCCACAAAAGTAAATGATCGTATAAGAAATTAACTACCAAC
			AAAAATCCCAAAGTTAAAGGAAGACATCCCCAAAAAAGATGTAACTTTCAAAACCGG
			ATGACTTCACTCCTGCCATTGCACCTAGTCATTTACTTCTCAGAGGAGTTTGGCCCT
			TTCTTCTTTCCAAAAGTAACCACTGCGGTAACAAACCGGCGGTTGTATTGCATTCG
			CTTGTAGGCGCGGCCTCTAGGCTTCTTCTTCTGTCTTGTTTGGCCACCTTAGGGTC
			CGC
SEQ ID NO:316	Middle	LPZ-307	GCGGACGCCTTGGTACAATGGACTTGCAAAAATAAAATGAGTTCTCATTTGTGGGT
			GAGATGCGGATATTTTATGCATAGGCACTTCATGGAGATGTGGTTTATAAACGCCA
			TCTTAATATCTGTACCTATTACTTTCAAAATATGAAGGCAAGATGGAAAGCTACTCAT
			CTGTTGTGAAGTCAGAATGTTGGTAGCGGTTGGGCTCTGAAAGTAAGAAACTTTTT
			GATTGGTTTAATTAAATGAGGGAATTTGCCTGGTTTCCCTCTTCCTTCCGAAAAAAA
			AAAAAAAAA
SEQ ID NO:317	Late	LPZ-308	GACGTTGTAAAACGACGGCCAGACAATATTGGAAGGGAGAAAGGCGCCAGCAGGG
			TTGAGGGGAAGAAATGCATAATGACATATATAATGAGATCTATTTGTATACGATATT
			ACGGGTACGATCGATGATTCGAGCTACGATCCCATACGACGCTAAAGCGTAATTAC
			ATATATAATAGATGCATTTCAGAATGACTTATCTATTTCATTACGCGATATTATATAC
			GTAATTACGTATATAATTGCAGAGATCTCACCGACCAACCAAATAGTCTTTCATTTC
			ATCCCAGGCGTCCGC
SEQ ID NO:318	Late	LPZ-309	GCGGACGCCTGTATCACTAGAGGTGAATACTCAGCAAGCAAAACTGAAGGATATTA
			TTGAAAAAGCTGTCAAGGCTAAATTGGGTGTCAATTCCCCATTGATCATGCATGGTT
			CTACACTTTTGTTTGAGTCCGGTGATGACATTGAGGAAGATGTTGCTGCACATTAT
			GCACAAAACTTAGAGAAGACGTTAGCAGAATTTCCAGTTCCAATCACAAATGGTGTT
			ATTCTTACAGTAGAGGACTACCAGCAAGAGTTCTTATGCAGTATTAATATTAAGCAC
			AGAGATGACTTTGATGAGGAGTCAGGTGGCATTGTACTGTCTGGAGGCGTCCGC
SEQ ID NO:319	Late	LPZ-310	GCGGACGCCTCCTTGTAGATACCATACATGAGTCTAAGATCAAAATCATACAAGAA
			GAGCTTCATTCCGGGCCTCACCTTTTCTACAAGCTCCTTTTTGGCTGGTGGAAAGC
			CAAACACTCTGTATCGGAAACACTCCTGCCTAGTTTCAGAATTACACATAAAAATCA
			AGCCGGCAAACCTATCTTTGCCACTGCCATCTTCATTGTTTGCGTCCTGGCCGTCG
			TTTTACAACGTC
SEQ ID NO:320	Late	LPZ-311	GCGGACGCCTTACTAAAACGACGGCCAGATGTGTAATGGGGAAAATGTGTCATGAT
			AGTTGGGTACAAATAACGAGCCACCTGCTCTATGTTTTCGAAGTTTTCTGTTGGATT
			TGTCCGGGTGAGAGAGCGTTCGTTCGTTGCGCGAGAGGGGCAAAATGCTGAGCG
			TGGGGAATTGCCATTGCCGCCCCTGGAAGTGCCGCACGAACGCGATCACATTTAA
			ATCACCATTTACTTCATCATCACCATGGTTAAATGCAGTCCCTGCTCCTTCAAACAG
			GAACTTCAGATCCTTCAAGCTCGAAATCTCCGCCTCTGCTTCCTCGAAGACAAGAC
			TCTGTGAGGAGGAAGCGCAGCAGCTGAGCTTAGCGGATCTGCTGAAGCCCGGTG
			GCCTCGCCCCCGATGGGTTCTCGTACAAGGAGAACTTTACCATACGCTGCTATGAA
			GTCCGAGTTAAACCGCACTGCCACCATTGAGGCGTCCGC
SEQ ID NO:321	Middle	LPZ-312	GACGTTGTAAAACGACGGCCAGCAACCAAATAAACCCCACATGTGCTCAATGTTTT
			AGTATAAAAGGAGATGACTTAAGAGTCATTTCACACACACTTCTATCTTGATTTCTCT
			CCACTTGTCTTGGGTTTTAGTGGAAGAGAAATCTAGGAGTGGAAGCCCTAGACGTT

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			GGAGGATAAGAAGGCAACCCTAGAAGGCAGAGCTAACGCTATCCTAAGGCAACCC
			TAACGCTATCCTAAGGCGTCCGC
SEQ ID NO:322	Late	LPZ-314	GCGGACGCCTGCTCAGCACCTGTTATAGTCATTTCTTTTTTCCTTTTTCTCATTTTTC
			TCTTTCGAATGACCGCAATGAAATTCAGGCTGCCCAACGCGTTTTTGTTTTCACAAT
			TAATTTTTGAATCATACGCGAAGATCATGATGAGAATGGTTGTGGAAAAAAACTGTT
			TGTAAATATTTAGGTGACCAACAATTTTCATGATTGCAATCTAAAGTTGATAATTGAT
			TTATCGGGTCGACATTTGTAATTATTAACACGGAAAATCTGAGGCTTACAATTTTTG
			GATTGTAAATATTTAGGTGACGAACAATTTTCATGATTGCAATCTAAAGTTGACAATT
			GAGTTATCGTGTCGACATTTGTAATTATTAACACACAAAATCTATGAGGCGTCCGC
SEQ ID NO:323	Late	LPZ-315	GCGGACGCCTCATCAATCCATGGTTGTACACGCGCCTTCAAAGCGGCTTCCTTATG
			TCGCGCAGCGTCTACTTGTTCCTTGAGCGCTTTTCCCTGCTACATCCGCGCGAGCC
			TCTGTGCAAGGGCCACTGTCTGCGCGGTCCCTTTAACTTCGTCGTACTTCTGCTGC
			AGCTCACGTGTCTCTATTTCTAAGTGCTATATATTTGGGTCCTCCTGCATAGTAGTG
			AACTTCGAACGACTCCTCAAATAGCCAGGTGTAGTCTTTCATTGCACTATTGATCTC
			CACTATTCCTGCTATAATGGCGCTAACATGCTGTTCCTTCACCTTTGGCGGAGTTG
			AAGGCTGCGCCTTCTTGGAGCTCGGTTATTTGAAGCTGAACCTTGGGCATATCTTC
			CTTCACCTCGTGCATCCCCTGCTTGGAGTTTCTGGATGCACGCCTCCACTGGGTCT
			TCTGCTGGGATGGGCAACTCTAAGACCAACTGGTATGCGTCGC
SEQ ID NO:324	Middle	LPZ-318	GCGGACGCCTTCTTCAATCCATCAGGCCTGATTAATGTATTGACCTTCTTTGTCTGA
			ATGTCATACATTTTTTTCACTGCATCCTTGATCTTCTTCTTGTCTTGCTTTCTATCCT
			TTCTCTTGCTTTCTATCCTTTCTCTGGC
SEQ ID NO:325	Late	LPZ-320	GACGTTGTAAAACGACGGCCAGCAAAATTGATATAAAGAATAGACACATCGACTCA
			AATGAAGTGACTCAACAGTTCATTAATTCATGTCAGCTTGAATGCATGGACATACAC
			CCATAAATAGGCAGTTGGGGTCACCCAAAAGAACATAGAAACATCTCGCATCTCTC
			TGAAGAAACTCGGATGGGTACAGGTCTGTGACTTCGCATATTTTGAAGGAGCACTC
			TCTTGGATAAGTACAATATAGGTACCATCTCGGACTCGCCTGAAATCTCGCAAAGA
			AGTCTCATTCTCCTCCTTGTTACAGGCGTCCGC
SEQ ID NO:326	Late	LPZ-321	GACGTTGTAAAACGACGGCCAGAAGCATCAATAAACAAAATGACAGATTAACAAGT
			TCTCTCTTAATCTTAAGAGAATACATCAACATCCAAGTAAAGTCATAACACATTTACA
			AAATGGTGCCACGGTATCCATTCTCTGTAACAAGGTTTTTCTGAAAATAGTTTTCCT
			CTTATCTATGTAACTCTTCATAGGGATGCCTGTGTCAACGTGCCATATTCCCAAATT
			TGGCCACAATCAAACCTTCCTCATTAGAAGAAACAATCTCTGGTCTAGCTCAAAATT
			GGCAAAATTTCCAGCATCTCCCTTTAACATCATTAGAAGGCGTCCGC
SEQ ID NO:327	Early	LPS-097	GGGAGATGCTAATTTGAAGCCCTTCTCTGAAGGTGGACAATTCCAGCAGCAGTGGT
			CTAAAGCCCCAATATGGCTATAGAAATTCTTCTGGGGGTTGCACCTATGGAAGAGG
			GTCGGAGAGGACGAAGCTGTGGATCGCTCTTACCATCTGTGCGGAAGGTGGTAGC
			AGAATTCATTGGAACGTTCTTCCTCATATTTGTAGGATGCGGATCTGTCGTTGTTGA
			TAAGATAAGCAACGGTTCCATAACTCATCTTGGTGTGTCGCTTGTATGGGGAATGG
			CGGCCATGATTGTAATTTATTCCATAGGCCATATTTCTGGAGCTCATTTGAATCCTG
			CAGTGACGTTGGCCCTTGCGGCTGTGAAGAGATTTCCATGGGTTCAGGTTCCAGG
			CTACATAGTAGCTCAAGTATTTGGATCGATATCTGCTGGGTTTCTCCTACGTTTCAT
			GTTTGGAGAAGTGGCATTCATGGGAGCCACAGTTCCTTCAGGCTCAGAAATGCAGT
			CTTTCGCTTTGGAAATTATTACTACGTCATTGTTGGTGTTTGTGGTTTCTGCAGTCG
			CCACTGATACAAAAGCGGTGGGTGAATTGGGAGGTTCAGCAATTGGAGCGACCAT
			CGCAATGAATGTAGCCATATCCGGACCAATCTCAGGAGCTTCAATGAATCCAGCAA
			GGACAATAGGATCCGCAGTGGCTGGCAACAAATATACAAGCATTTGGGTTTACATG
			GTTGGGCCTGTAATCGGTGCGCTAATGGGTGCAATGAGTTATAACATGATTAGAGA
			GACAAAAATGTCCGAAAGGGAGATTATGAAGAGTGGGTCATTTGTTAAGGACATGG
			GCTCCAGCGAATCAACAGCATAACAACTTAGAGATTTNTTGCATTCCCGAGACGGT
			ATCCAGTGATAGTGGAGAGTAGTCATAATAAGATTTGTGAAAATGTTTGTGTAGATT
			AATGTGTAAAATTCAATCCATCAACCATGAAGCGAACTGCATTCCGTTTTTAAATGT
			TTATTGGATTTGAATTAATAAACAGCTTATACGTGAAAATCCCTACTTTATGTACGGA
SEQ ID NO:328	Early	LPS-098	ACTATAGGGCACGCGTGGTCGACGGCCCGAGCTGGTATCCGATGAAGCTAGATTC
			AATGGTTCAAGTCCTATGAAAGCTAGATTGGAGAATTGCAAAGAAATCTAATCTCCG
			TTAGTTGTCCCAACCACTGACTCGCACCCAATCAGAGTATATTAAAGTTAAAGATTA
			TATAAAGGTAAATTGAACATTTATAAAATCTTAAATGTATTTTTAGAGTTAAACATTAT
			ATAGAATATTTAATGTAGTATAGATATAATAAAATATTAAAAATTAATTTCTCTTTACT
			ATCAAGTGAATAAAAATAAAAAATAAATGTAAGACAATATAATAAAAGACTTGTTTTT
			AGTGCATTTTTTGGACTCTTCGTTATTGTGTGGTATTGTGTTATTTAAACTGATCTTT
			TTACTGTATATATGGATGGGTTACCCATCAAACTTGTGATTTCAATAAATTCCTCCC
			GGATTTTAGAGAAATTAGACCATAAAAACTCACGAAAAAAATTTTAGACCATAAAAAC
			TCACGAAAAAAACTTCCCCAAAATCACGCTAAAAACAACTAGATAAAAAAATACCCA
			TCTTTGATGATGTGGATAGTGACAGCCTATTCCAAACTATCACCTAAATTGTAAGTT
			ACATGCATAACACGATGACCTCATCTATACGTTGTGCCAAATAAAGGTATGACCGTT
			CAAACTAAAGAATCAACGAGCTCCAACGCATCTTTTGCTGTGGGGGGATTCTCACG
			GCTTAACATTCATGGANCCGATTACCTTNCTANCCAACCAAGGGTTTTAACCTGG
			CAAATNCCAAACCAATTACCAGCTTNACAAATCAACCGAGCCGCCCNACCGGGATC
			ATTTTGGTCAAGTCTCGAAAACNGGCATTGGGTATATGGNATATGGAATTGGAATT
			GGATCAATGGTAACCTTGGGANAAGCTTAANTTGGAAANCCCTTTTTTTTGANGGG
			GGCCAANTTCCCGNNCCCCCGG
SEQ ID NO:329	Early	LPS-099	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCTATGGTCGACCTGCAGG
			CGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATGCACAGCTTCGTCCTCT
			CCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGGC
			TTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCAT
			CTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGACT
			GACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTCA

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			GTTAAAGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCCT
			CACAGCAAAAGATGCGTTGGAGCTCGTTGATTCTTTAGTTTGAACGGTCATACCTTT
			ATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAATTTAGG
			TGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTATC
			TAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTAAAA
			TTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGGGAGGAATTTATTGAA
			ATCACAAGTTTGATGGGTAACCCATCCATATATACAGTAAAAAGATCAGTTTACCAG
			CCCGGGCCGTCGACCACGCGTGCCCTATAGTAATCGAATTCCCGCGGCCGCCATG
			GCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGTCGTATTAC
			AATTCACTGGCCGCGTTTACACGTCGTGACTGGGAAACCCTGCGTTACCACTTAAT
			CGCTTGAGCACATCCCCTTTTCCAGTGNGTAAAACGAAAAGGCCCCNCCATCGCCT
			TTCAAAAATTGGCAACTGAANGGGAAGGACCCCCT
SEQ ID NO:330	Early	LPS-100	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAG
			GCGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCC
			CTCCGACCCTCTTCCATAGGTATAAAACCCAGAATTTGGTGAGCAGGAAGAATTTC
			CATAGCCATATTGAGGCTTTACACCACTGCTGCTCGAATTGTCCACCTTCAGAGAA
			GGGCTTCAAATTAGCATCTCCAAGTTACATGGATCTATTCTATTCATATATTTATAAC
			AATGCTGCTTCGAGACTGACAAAATTATTTGTTGGCGCTTGTTCATCGTTAGCTGTA
			ATGGTTTGGATTGTTCAGTGTAGGACCAGCCCGGGCCGTCGACCACGCGTGCCCT
			ATAGTAATCGAATTCCCGCGGCCGCCATGGCGGCCGGGAGCATGCGACGTCGGG
			CCCAATTCGCCCTATAGTGAGTGGTATTACAATTCACTGGCCGTCGTTTTACAACGT
			CGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCC
			TTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAG
			TTGCGCAGCCTGAATGGCGAATGGACGCGCCCTGTAGCGGCGCATTAAGCGCGG
			CGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGC
			CCGCTCCTTTCGCTTTCTTCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTC
			AAGCTCTAAATCGGGGGCTTCCTTTAGGGTTCCGATTTATGCTTTACGGCACCCT
			CGACCCCAAAAAAACTTGATTAGGGGTGATGGGTCACGTAGTGGGCCATCGCCCT
			TGATAGACGGTTTTTCGCCCTTTGACGNTGGAAGTCCACGTTTNTTTAATAGNGGG
			ACTCTTGGTTCAAAATGGGACAACACTTCAAACCTTTTTTGGGGNTATTTTTTTTGAT
			TTATNAAGGGATTTTTGCCGNNTTTNGGGCCTTTTGG
SEQ ID NO:331	Early	LPS-101	ACTATAGGGCACGCGTGGTCGACGGCCCCGGCTGGTTTCAATAAATTCCTCCCGG
			ATTTTAGAGAAATTAGACCATAAAAACTCACGAAAAAAATTTTAGACCATAAAAACTC
			ACGAAAAAAACTTCCCCAAAATCACGCTAAAAACAACTAGATAAAAAAATACCCATC
			TTTGATGATGTGGATAGTGACAGCCTATTCCAAACTATCACCTAAATTGTAAGTTAC
			ATGCATAACACGATGACCTCATCTATACGTTGTGCCAAATAAAGGTATGACCGTTCA
			AACTAAAGAATCAACGAGCTCCAACGCATCTTTTGCTGTGAGGATTCTCACGGCTA
			ACATTCATGACCGATTACCTCCTACCAACAAGGCTTTAACTGAACAATCCAAACAAT
			TACAGCTAACAATCAACGAGCGCCAACGGATCATTTTGTCAGTCTCGAAGCAGCAT
			TGTTATATGTATATGAATAGAATAGATCAATGTAACTTGGAGATGCTAATTTGAAGC
			CCTTCTCTGAAGGTGGACAATTCCAGCACCAGTGGTCTAAAGCCTCAATATGGCTA
			TAGAAATTCTTCTGGGGGTTGCACCTATGGAAGAGGGTCGGAGAGGACGAAGCTG
			TGGATGCTCTTACCATCT
SEQ ID NO:332	Early	LPS-102	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAG
			GCGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCTC
			TCCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGG
			CTTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCA
			TCTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGAC
			TGACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTC
			AGTTAAGGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCC
			TCACAGCAAAAGATGCGTCGGAGCTCGTTGATTCTTTAGTTTGAACGGTCATACCT
			TTATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAATTTA
			GGTGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTT
			ATCTAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTA
			AAATTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGGGAGGAATTTATT
			GAAATCACAAGTTTGATGGGTAACCCATCCATATATACAGTAAAAAGATCAGTTTAA
			ATAACACAATACCACACAATAACGAAGAGTCCAAAAAATGCACTAAAAACAAGTCTT
			TTATTATATTGGCTTACATTTATTTTTTACTTTTATTCACTTGGATAGTAAAAGAGAAA
			TTAATTTTTAATATTTTATTATATCTATACTACATTAAATATTCTATATAATGTTAACTC
			TAAAAAACATTTAAGATTTATATATGGTCAATTACCCTTATATAATCTTTAACTTTAAA
			TCCCTGATGGGGGCCAATAANGGTNGGGAAACTAACGGAAN
SEQ ID NO:333	Early	LPS-103	ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTTTCAATAAATTCCTCCCGG
			ATTTTAGAGAAATTAGACCATAAAAACTCACGAAAAAAATTTTAGACCATAAAAACTC
			ACGAAAAAAACTTCCCCAAAATCACGCTAAAAACAACTAGATAAAAAAATACCCATC
			TTTGATGATGTGGATAGTGACAGCCTATTCCAAACTATCACCTAAATTGTAAGTTAC
			ATGCATAACACGATGACCTCATCTATACGTTGTGCGAAATAAAGGTATGACCGTTCA
			AACTAAAGAATCAACGAGCTCCAACGCATCTTTTGCTGTGAGGATTCTCACGGCTA
			ACATTCATGACCGATTACCTCCTACCAACAAGGCTTTAACTGAACAATCCAAACAAT
			TACAGCTAACAATCAACGGGCGCCAACGGATCATTTTGTCAGCCTCGAAGCAGCAT
			TGTTATATGTATATGAATAGAATAGATCAATGTAACTTGGAGATGCTAATTTGAAGC
			CCTTCTCTGAAGGTGGACAATTCCAGCACCAGTGGTCTAAAGCCTCAATATGGCTA
			TAGAAATTCTTCTGGGGGTTGCACCTATGGAAGAGGGTCGGAGAGGACGAAGCTG
			TGGATCGCTCTTACCATCT
SEQ ID NO:334	Early	LPS-104	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCTATGGTCGACCTGCAGG
			CGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCTCT
			CCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGGC

TABLE I-continued

cDNA	Embryo Phase	Clone	Nucleotide Sequence
			TTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCAT
			CTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGACT
			GACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTCA
			GTTAAGGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCCT
			CACAGCAAAAGATGCGTTGGAGCTCGTTGACTCTTTAGTTTGAACGGTCATACCTT
			TATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAGTTTAG
			GTGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTTA
			TCTAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTAA
			AATTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGAGAGGAATTTATTG
			AAACCAGCCCGGGCCGTCGACCACGCGTGCCCTATAGTAATCGAATTCCCGCGGC
			CGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGT
			CGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGCG
			TACCCACTTAATCGCCTTGGAGCACATCCGCCTTTCGCCAGCTGGCGTAATAGCGA
			AGAGGCCCGGACCCGATCGGCCCTTTCCAACAAATTGCGCAACCCTGAATNGGGA
			AATGGGCCCCCCCCTNTTACCGGNGCAATTAAACCCCGGGGGGGNGNGGGGGTT
			CCCCCCCCCGTGGACCT

TABLE II

Clone	SE1–SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPS001	0	249.4	1400.9	827.6	1683.8	2019.4	189.2	4303.9
LPS003	701.2	555.9	2815.2	2445.1	3249.9	3094.7	227.1	3111.6
LPS004	466.1	335.5	2652	2701	2644	2329.6	218.5	2332.4
LPS006	753.1	332.7	3287.3	2964.5	2832.2	2688.9	182.1	1591.9
LPS007	685.2	226	2010.2	1911.3	2600.4	1730.1	181.5	2737.7
LPS008	652.8	274.8	2415	2219.3	2607.1	2294.9	155.7	1292.1
LPS010	558.3	356.1	2667.6	2881.1	2584.3	1573.4	161.7	1041
LPS011	3536.1	424.7	4021.5	3793.8	3590	3182	160.5	1471.7
LPS012	809	408.4	2206.7	2187.1	2282.2	2422.5	462.4	1483.2
LPS013	1211.1	391.6	2294.7	2652.6	2005.4	2167.8	166.8	1570.5
LPS014	2191.9	432.5	2651.8	3013.5	3341.2	3586.7	178.8	3527.1
LPS015	1197.9	306	5651.4	14828.6	20242.8	21558.2	1427.2	34472.3
LPS019	1830.2	334.5	3329	3954.4	4347.5	4658.2	312.1	4743.1
LPS020	675.2	327.8	2258.3	2284.7	2542.7	2321.4	171.9	1609.8
LPS023	451.3	337.5	1401.9	1106.8	1766.2	1842.6	109.6	1365.2
LPS024	4585.8	444.5	3006.3	3431.1	3548.8	3759	157.3	4062.3
LPS025	5102.3	397.1	4322.9	4699.6	5067	4973.2	262.4	5240.4
LPS026	1568.7	285.9	1809.9	1830.4	2829.9	2381.7	164.9	1404.9
LPS027	5499.9	458.4	4853.9	5218.6	2598.4	1756.6	457.9	2375.3
LPS028	4812.9	314.9	2368.8	2616.5	3113.3	3292.4	557	4146
LPS029	4464.6	251.2	2334.4	2058.1	2930.3	3219.3	472	3814.4
LPS030	1142.2	352.5	2519.8	2460.9	2499.8	2634.5	378.3	2147.8
LPS031	1067.7	481.6	3510.8	2799.2	3568.2	3257.2	287.9	2209.7
LPS032	1120.2	332.3	3153.1	3032.4	1769.2	1816.7	146.6	2689.9
LPS036	1498.2	1072.9	4633.6	5524.2	5465.1	6350.7	918	14058.5
LPS037	1890.3	320.9	3719.1	3618.9	4138	4518.1	513.4	5087.5
LPS038	2899.5	310.3	4530	4226.1	4491.6	3969	268.4	4245.3
LPS040	527.4	238.1	1433.4	1611.2	1984.5	1506.5	143.9	1988.7
LPS041	506.1	265.5	1958.9	2843.2	2065.3	2016.2	147.4	2781.7
LPS042	1432.1	1140.3	4379	4973.3	4525.4	4340.8	319.6	3009.8
LPS043	696.9	776.2	3933.1	4894.3	3512.2	3664.7	340.6	3098.4
LPS044	57.8	275.1	3365	4261.2	4773.5	4979.9	974.4	10645.5
LPS045	536.1	211.1	1559.5	1415	1498.5	1584.8	562.1	1912.3
LPS046	796.3	231.7	1023.9	306.4	1417.8	1328.2	83.8	946.4
LPS047	5029.9	518.2	3632.5	4262.1	4755.5	4087.9	386.3	4933.8
LPS050	6333.5	2620.8	5271.4	5242.1	5586.4	5560.1	980.1	11444
LPS051	1378	224.4	2328.8	2221.8	2260.5	2715.1	123.7	3670.4
LPS052	1526.4	267.5	2046	1856.2	2186.5	2416.3	99.3	2010.1
LPS053	4438.3	361.6	4087.6	3959.9	4786.5	3666.8	379.6	4256.7
LPS054	1992.9	269.9	2734.2	2388.1	3143.8	2337.7	177.6	2803.9
LPS055	4587.8	334.4	3488.6	3474	4018.3	3101.6	196.2	4309.4
LPS056	5960.7	1333.7	5338.8	5670.3	5674.4	5533.5	446.4	5593
LPS057	2219.9	301.9	2397.3	2356.1	2218.1	2085.6	184.4	2657.8
LPS058	4070.4	299.9	3485.4	3721.3	4113.8	4142.2	239.8	4945.6
LPS059	8729.3	279.2	3885.7	3636	2720.4	3346.7	165.7	3734
LPS060	4580.2	323.7	3027.8	4713.4	4929.1	5047.5	161	4704.8
LPS061	2831.9	366.8	2392	2327.7	2546.5	1991.8	177.9	3036.7
LPS062	1674.1	353	2711.2	2526.1	1847	1830.3	124.5	3584.2
LPS063	5514.4	419.8	5238.9	5020.3	5417.4	5041	250.1	4812.6
LPS064	7417	3166	5229.5	7497.4	7933.1	10261	1088.3	16829.6
LPS065	5634.9	343.5	5527.8	5099.4	7833.4	5356.6	237.5	4696.7
LPS066	1015.9	244.5	1702.6	1650.5	2895.1	2437.2	128	2514.1

TABLE II-continued

LPS067	2796.8	240.4	3931.5	4810.3	5407.8	5418.3	202.5	9403.8
LPS069	533.4	189.9	1635.8	1816.4	2114.2	1646.8	119.8	3208.8
LPS070	2516.9	240.6	1909.5	2519.6	2156.7	1777.4	186.4	4362.1
LPS071	592.8	196.4	1789.2	2189.2	1981.1	1304.5	127.6	3430
LPS072	444.2	217.6	1422.9	1509	2065.3	2289.9	122.7	2678.8
LPS073	4362.8	273.1	3094.9	3348.1	3771.8	4075.3	137.7	4259.6
LPS074	32072.9	6816.3	33531	25258.9	38176.4	32687.7	14607.1	37529.6
LPS075	7013.9	472.7	4759.7	4933.9	5452.2	5408.7	409.4	5397.1
LPS076	4236.1	362.6	3131.9	2882	3368.5	3354.6	119.5	3141.9
LPS077	2958.7	276.6	4380.4	4862.5	4475.1	4958.7	218.9	4426
LPS078	23685.3	2642.5	35458.6	25869.6	42378.9	33047.1	25402.2	37189.8
LPS079	4794.3	547.8	4628.6	4821.8	5257.2	5277	829.5	5449.7
LPS080	30454	10527	33713.7	23785.4	32590.9	32210.7	16224.4	37659.2
LPS081	30405.9	28677	35358.3	25873	22338.1	31715.3	36436.4	36650.5
LPS083	5040.1	460.8	3251.7	3487.3	2688.9	2565.9	190.5	2979.7
LPS084	2031	298.9	2843.7	2718.4	2352.2	2165.5	164.9	3398
LPS086	3571.7	320.1	2715.8	2648	1989	2528.4	143.9	2969.7
LPS087	3302.3	337.4	4873.1	5695.8	5407.2	5450.6	670.8	18404.9
LPS088	826.8	302.1	2389.2	2871.1	3180.8	2635.2	138.6	3141.5
LPS089	796.4	321.2	1987.7	2640.6	3299.1	2285.1	143.7	3176.6
LPS090	4031	235.9	3867.3	4064.4	4503.3	4798.4	341.7	4697.7
LPS091	2423.3	196.5	2836.8	3101.3	4049.1	4172	295.2	4612.2
LPS092	2914.9	208.5	4005.3	3138.4	3911.6	4036.1	270.4	4842.9
LPS093	793	195.5	1619.2	1331.6	1909.3	1843	147.1	2772
LPS094	1374	221	2205.5	2028.5	2240.9	2632.2	163.3	2849.1
LPS095	728.7	174.1	2022.6	2112.1	2335.8	1264.6	117.5	2957
LPS096	393.3	168.5	1531.9	1393.4	1893.3	869.1	118.3	1691.1
LPZ001	2008.6	185.4	2535.9	2937.9	3472	1981.8	118.9	2421.7
LPZ002	3529.3	384.6	4579.3	4474.6	3236.7	3855.8	313.8	3237.5
LPZ003	4076.8	275.4	2651.2	2966.7	2829.2	4177.4	378.5	4369.7
LPZ004	5595	687.4	5468.2	5615.9	5243.6	5699.6	601.6	5889.9
LPZ005	5680.5	3353	34994.7	26121.9	42555.1	33144.5	16193.7	37798.2
LPZ006	1199.8	299.4	3013.7	3099.8	3517.3	3397.1	140.6	3370.8
LPZ007	1159.1	462.2	3292.7	2992.5	3121.4	2936.7	235.5	3238.6
LPZ008	1874.3	237.7	3110.8	3236.7	2516.5	3182.2	325.3	4330.1
LPZ009	3331.1	296.3	2348.5	3414	2478.2	3309.5	348	5658.1
LPZ010	3216.3	1186.8	4977.3	5024.7	4564.4	4992.4	442.6	4454.5
LPZ011	4613.4	910.9	4510.7	4515.7	3729	4357.3	371.4	4695.9
LPZ012	1531.5	469.5	2915.3	2611.1	2012.3	3481.4	270.3	3804.3
LPZ013	3495.1	268.8	2125.9	2584.7	3194.7	3787.4	125.1	4929.6
LPZ015	2040	257.6	1971.1	2966.7	2191.1	3056.7	227.1	4156.6
LPZ016	5307	2761.1	8451.7	17219.7	22792.7	15567.3	1073.6	35074.1
LPZ017	2476.4	354.3	3175.5	4330.8	4496.2	4061	273.2	5328.9
LPZ018	3929.4	417.5	12420.2	14916.1	18116	17637.5	2541.6	31981
LPZ019	5404.2	427.3	32190.3	24710.4	42102.7	32342.6	19528	36969.5
LPZ020	576.9	142.9	1451.4	1505.4	3534.8	2679.8	210.9	3046.2
LPZ022	1408.2	155.2	2406.7	2845.7	3042.5	3074.8	189.9	3829.2
LPZ023	562.1	152.8	2096.7	1710	2045.5	2078.9	200.8	2874.3
LPZ024	496.7	158.1	1681.3	1264.7	2102.9	1857.1	132.1	1818.4
LPZ025	5431.3	464.1	13492.2	9726.2	11911.5	13462.8	1262.5	11780.6
LPZ026	1663.2	139.7	2464.8	2760.1	3113	2219.4	159.1	3183.5
LPZ028	5029	190.7	5367.2	5339.8	5483.9	5205.5	482.3	5565.9
LPZ029	961.3	119.2	1805.4	1989.6	2298.5	1998.4	126	2576.9
LPZ030	1457.4	177	2444.7	2687.5	1966.4	1857.2	178.5	3312.8
LPZ031	3092.8	361.7	3564	3925.3	4627.8	5171.4	506.7	5920.5
LPZ032	1906.5	156.8	5542.3	24342	42917.8	33386.1	30058	37998.6
LPZ033	12934.5	354.7	5280.1	7301.2	5638.9	9238.7	375.4	15843.5
LPZ034	1307.4	177.5	1737	2208.4	3213.1	1984.1	150.2	3228.3
LPZ035	556.5	201.9	880.2	1280.1	1654.5	915.1	74.1	1422.1
LPZ037	1356.8	269.7	2072	3110.5	2912.8	2488.2	211	4119.3
LPZ038	4027.9	426.9	5639.9	5872.3	5476.8	5614.6	796.8	5583.3
LPZ039	5059.1	550.6	3807.9	4393.8	3825.6	3889.8	342.2	5164.2
LPZ040	1226.1	236.5	1566.4	1889	1679.1	2263.6	140.6	3331.1
LPZ041	944.2	219.3	1629	543.1	1148.2	1416	90.2	2524.6
LPZ042	570.6	206.1	1129.5	806.5	1448.8	1423.1	75.1	2013.8
LPZ043	1190.2	236.7	1878.8	1024.4	2834.6	2767.4	241.7	3236.2
LPZ045	5315.3	465.7	4933.2	5580.2	5151.1	5205.1	557.3	10754.3
LPZ047	859.5	285.2	1606.2	2099.3	2059.4	1992.6	68.3	3054.8
LPZ049	3232.7	108	1278.6	2834.2	3657.8	3944	244.2	5459.6
LPZ051	3048.1	146.9	2373.2	2067.3	2745	2383.2	179.1	2837.6
LPZ053	2580.3	135.6	2625.8	2088.7	2468.5	2297.2	156.8	3001.4
LPZ054	1838.1	159.5	2657.8	2759.7	2658.1	2224.7	170.4	3444.2
LPZ055	2181.8	151.1	2381.2	2262.7	3228.3	2983.9	139.3	2673.9
LPZ056	4028.3	219.5	2884.6	3416.6	3779.6	3789.9	208	4518
LPZ057	1470	121	1676.5	1629.6	1702.7	1703	112.2	2272.1
LPZ058	1923.3	122.5	2453.5	2169	3127.3	2465.4	160.6	3319.6
LPZ059	1760.4	113.8	2180.6	1832.4	1997.2	1530.8	174.4	3366.6
LPZ060	3296.4	139.3	2571.1	2250.2	2721	2976.9	221.3	3898.5
LPZ061	2495.6	182.8	2663.9	2235	3265.9	4227.1	498.1	4915.1

TABLE II-continued

LPZ062	1992.7	194.9	3296.7	3975.8	3861.5	5642.6	497.6	5606.2
LPZ063	2167.1	145.9	2733	1843.9	3066.6	4961	305.6	4773.2
LPZ065	5641.2	251.7	13690.3	9269.2	8562.8	13254	986.3	9554
LPZ066	6307.3	652.4	12630.8	6968.4	4918.9	5062.2	400.7	5456.8
LPZ067	10838	1548.1	16986	11776.8	5633.2	7054	1014	15262.2
LPZ069	1481.9	209.6	2239.8	1480.9	2496.7	2542.4	250.5	3717.2
LPZ070	1932.5	263.8	1895.1	2221	1555.9	1570.4	145.5	3471.3
LPZ071	3672.6	378.6	4185.5	3050.5	4166.8	4246.2	553.7	5333.4
LPZ072	744.5	210	1210	676.7	1420.2	1393.4	95.8	1997.1
LPZ073	1997.9	235.9	2275.1	2141.7	2613.2	1989.9	170	3489.4
LPZ074	1375.9	237.4	1899.1	1787.3	2472.9	1623.7	125.6	2435
LPZ075	831.4	247.9	1536.4	1773.1	1886.9	920	80.6	1053.5
LPZ076	345.7	251.8	854.8	564.6	1747.1	526.2	55.9	1058.3
LPZ077	2466.3	102.2	949.4	820.9	3093.9	3179.6	202.9	3314.8
LPZ078	3102.1	197.1	3654.2	3261	4204.3	4433.6	400.8	5559
LPZ079	1584.4	108.3	2389.2	2243.3	2624.8	2677.1	208.3	3675.6
LPZ080	12206.5	2043.1	25021.4	8579.5	11707.8	8717.6	1172	18663.9
LPZ081	1368.7	103.6	1902.8	1349.9	2166.1	1597.7	103.5	2709.6
LPZ082	2601.3	140.3	3264.3	2853.9	2799.6	1742.3	251.1	4288.2
LPZ083	1311.9	76.7	1622.4	1071.1	1733.9	1878	104	2007.7
LPZ084	9974.7	801.3	14255.3	8399.1	5763.9	8852.9	542.2	5714.3
LPZ085	4609.8	158.4	3923.3	3729.7	4082.8	3867.3	219.3	4075.1
LPZ086	10874.1	987.4	19189.5	8284.6	5646	9109.8	1116.4	14988
LPZ089	3505.8	211.6	4010	3430.6	3762.1	3770.8	224.3	5341.2
LPZ090	5780.9	581.8	13217.4	6303.4	4694.8	4779.9	425.2	5408.9
LPZ091	5316.1	148.4	2263.4	2139.8	2382.2	4067.2	256.8	14732.6
LPZ092	5448.7	209.4	3631.6	4152.7	2934.1	3403.7	174.9	4943.6
LPZ093	1169	159.4	2097.9	1187.4	2050.8	2350.7	109.4	2605
LPZ094	1245.5	139.7	1547.5	1650.5	1875.2	2009.9	80.2	2376.9
LPZ095	711.2	177.9	900.9	1253.3	1013.8	1395.3	48	1586.1
LPZ096	2122.2	249.7	2929.3	3271.3	2132.9	2224	232.8	4443.8
LPZ099	4306.4	211.2	2603.1	2144.4	3479.2	3488.5	138.1	4085
LPZ100	3373.5	297	3941.3	3149.6	3790.4	3857.5	443.8	5028.1
LPZ101	3007.7	272.4	3546.9	2291.3	4299	3232.1	306.1	4819.6
LPZ102	2092.7	324.7	3167.5	2109.3	3524.3	2829.4	279	4297.4
LPZ103	3602.1	285.7	2923.3	3112.9	2812.9	1318.3	87.9	1739
LPZ106	1359.7	305.1	2680.3	2391.6	2838.5	2097	173.7	3009.6
LPZ107	28560.8	4989.5	20821.7	17880.4	39173.1	27035.1	11973.3	36123.4
LPZ108	4136.8	179.4	4259.8	4978.2	5553.2	4862	837.2	5597.5
LPZ109	3708.3	202.4	3842	3510.4	4638.4	4453.7	469.5	5107.4
LPZ110	4557.2	291.4	5020.6	4801	4487.4	4481.1	552.3	5484.2
LPZ111	1625.6	130.9	2242.1	1982.7	2740.6	2455.4	164.6	3722.3
LPZ112	2887.4	195.8	3813.2	3759.4	3984.8	4167.1	409.7	5461.8
LPZ114	5029.5	213.4	5016.7	4678.8	5036.9	5168.1	302.1	4316
LPZ115	24434.4	2637.1	27958	23684.2	41104.3	30920.9	2153.9	36902.6
LPZ116	8682.9	235.7	5647.3	5316.6	5805.6	9313.7	466.6	16018.9
LPZ117	30879	4843.7	36277.1	24358	24673.1	20545.7	4669.9	5652.6
LPZ118	4023.6	171.1	3743.5	4568.2	3845.4	3783.9	254.3	4782.5
LPZ119	2580.4	114.1	2507.2	3114.1	2544.6	1963.8	127.6	3195.4
LPZ120	1998.8	157	1987.2	1503.1	2331.8	1805.1	131.5	3522.3
LPZ122	2041.4	119.6	2145.6	2430.9	1998.6	2171.8	101.3	2677
LPZ124	2795.6	185.4	2980.4	2672.5	2495.2	3459.4	173.1	3081.5
LPZ126	2559.7	181.8	2560.1	2349.8	3500.6	2362.1	224.9	3646.9
LPZ127	1993.5	169.1	3161	3180.8	3382.5	3321.3	180.6	4058.4
LPZ128	2866.7	263.2	3556.8	3597.4	3545.7	3813.8	306.7	4071.3
LPZ131	1993.5	171.7	1983.9	2069.6	2565	2607.2	80.3	2527.8
LPZ133	2446.7	290.4	3218.6	2847.2	3830.1	2889.5	245	4252.4
LPZ136	1952.3	281.1	2956.9	1870.6	3167.6	2680.6	215.9	4291.6
LPZ137	2833.8	281.9	3264.4	2350.2	3874.4	3532.8	420.8	4935.3
LPZ138	2932.9	1791	5211.5	4502.1	5409.9	4832.8	543.1	4741.3
LPZ140	2284.7	337.4	3680.2	2810.9	3196.1	3191.2	271	4613.6
LPZ141	4726.2	368.5	4792.5	4412.5	5368.1	5466.3	722.1	4956.4
LPZ143	25290.6	2692.2	35967.9	25679.9	43668.3	32612.1	25456.9	36344.4
LPZ144	2620.9	286.6	3948.7	3394.6	4505.7	4142.8	488.7	4776.7
LPZ145	3472.5	171	3949	3194.2	3430.5	3539.9	327.9	4487.2
LPZ146	2612.8	127.3	2482.4	2080	3000.8	2979.1	135.1	3391.3
LPZ147	2447	106.3	2855.1	2237.7	3134.2	2841.8	261.6	4388.1
LPZ148	2036.8	77.7	2559	1932.3	4296.1	4699	359.6	3982.3
LPZ149	5720.7	267.4	5377.3	5408.2	10999.7	5717.7	1078.9	13033.2
LPZ150	5861.7	772	35541.7	26314.8	44633	33238	13126	37853.6
LPZ151	5550.3	3499.3	9012.8	8380.4	11968.1	5716.5	715.8	5536.9
LPZ152	4746.6	352.8	5169.3	5647.7	5384	5394.2	408.5	5382.1
LPZ153	21881.2	2773.2	14738.2	15979.5	16996.8	15756.8	2388.5	30812.9
LPZ154	4869.8	265.9	3244.3	3497	3948.6	3703.3	303.8	4119.1
LPZ155	3904.2	1596.3	5078.5	5482	4631.7	5314.1	553.4	4112.9
LPZ157	4726.5	1732.8	5427.1	5369.5	5213.3	5705.9	756.4	5462.2
LPZ158	15297.4	3817.1	17993.9	17405.3	25168.8	22056.6	2337.4	22375.3
LPZ162	5725.8	4204.8	10380.1	11364	17948.2	14250.8	1934.6	10535.5
LPZ165	5615.2	666.7	5274.6	5486.6	5560.3	5310.9	637.1	5405.9

TABLE II-continued

LPZ166	5889.1	2603	9503.5	10943.7	13743.3	14080.4	1772.5	5772.8
LPZ167	5347.2	1948	5708.9	6769.6	5742.3	5347.9	370	5279.7
LPZ169	3043.8	267.4	1976.6	2851	3451	2451.2	189.8	3420
LPZ170	3507.3	301.5	3532.3	3391.4	4481.4	3398.7	130.2	5604.2
LPZ171	3762.3	780.7	4554.8	4311.7	4936.4	4511.3	398.6	5030.5
LPZ172	5098.2	947.4	5550	6287.9	5135.4	5323.9	1242.5	8539
LPZ173	22580.5	3313.9	35486.9	24974.9	42874	31828.8	26531.8	36066.9
LPZ174	4115.7	221	5241.5	4262.4	5765.8	5554.9	872.5	4815.2
LPZ175	4388.3	1360.6	5563.7	5504.9	5165.3	5182.9	583.2	4602.3
LPZ177	1371.6	94.5	2119.4	2218.6	2730.7	2431.7	143.2	2893.2
LPZ179	3643	195.1	4409.9	4898	5458.3	5319.8	797.9	5677.7
LPZ181	5573.3	215.9	4799.6	5272.2	5825.3	5554.4	1573.5	13689.7
LPZ182	4118.9	107.6	3491.5	3182.1	4617.5	4543.6	478.1	5527.8
LPZ186	5792.2	325.5	4965.1	5182.6	12373.6	11191.4	1804.9	37336.4
LPZ189	33820.3	5188.5	30941.4	24955	43453.2	33115.2	17929.3	38055.6
LPZ194	2807	151.1	2915.9	2955.1	3306.8	3120.2	142.9	4101.6
LPZ195	5345.7	532.7	5597	5628.7	5540.4	5491	545.7	5756.7
LPZ196	4805.1	3512.9	5183.2	6968.6	5465.4	5052.4	786.4	5694.5
LPZ197	7268.6	159.8	5398.9	5673.5	13582.6	15111.9	3499.6	34684.8
LPZ198	7208.3	210.6	5800.8	8043	5439.2	5183.6	409.3	5042.7
LPZ199	3058.3	186.1	2749.6	2667	3713.6	3704.3	243.4	3917
LPZ201	7175.3	236.7	4827.6	5029.9	5523.4	5802.2	1981.9	14614.5
LPZ202	3603.3	1113.9	35531.5	26035.1	44762.8	33837.3	63521.8	38225.4
LPZ203	4325.4	424.4	5517	5387.3	9934.8	5662.1	2104.8	9370.7
LPZ204	32355.9	34690	36443.6	26004.3	44546.1	33680.5	55702.6	37890.3
LPZ205	4904.1	519.6	5162.4	5398.7	5427.6	5325.6	281.4	5770.2
LPZ206	3504.4	319.8	3124.8	4561.7	4192.2	3899.9	255.7	5489.9
LPZ207	32035	24978.7	34825	23371.8	42639.9	32686.4	30672.2	37674.8
LPZ208	25174.6	3118.6	14244.4	13906.3	16694.7	21111.9	2190.1	34542.4
LPZ210	3885.1	422.3	3895.8	4551.5	4205.7	5108.7	258.6	5514.3
LPZ211	2569	176.7	3689.2	2943.5	4001.9	3860.9	250.2	3113.1
LPZ212	5988.8	1244.3	32684.4	11154.1	19853.4	13654	618.3	10736
LPZ213	3406.9	106.8	3964.1	3876.6	4236.4	4294.4	274.2	4874.6
LPZ214	1668.3	55.3	2136.3	2394.8	2390	2269.3	105.8	3436.2
LPZ215	5019.8	139.3	5020.1	5024.8	11013.9	13747.1	1991.7	36930.6
LPZ216	3336.8	1085.4	35895.6	26245.3	44980.1	33834.4	64482.7	38238.1
LPZ217	23512.1	26363.3	36065.8	24685.4	43193.4	31422.4	21462.1	35990.6
LPZ219	4011	256.9	3193.5	3326.3	4509.5	5258.5	455.2	5841.9
LPZ220	8696.5	2383.3	5064.7	5171.3	4923.7	5340	951.7	17530.6
LPZ221	1221.4	83.1	1201.8	707.6	1556.5	2083.9	182.1	3948.8
LPZ222	1885	146.1	2834.7	2253.2	2557.7	3382	196.7	4225.1
LPZ223	1048.5	121.2	2339.6	2642.1	2663.8	3573.5	383.5	4579.2
LPZ224	3190.6	118.8	3049.8	2833.2	4373.8	5139.9	858.6	5285.7
LPZ225	25428.2	4079.7	35724.5	25423.6	43300.5	32574.8	38888.3	37219.9
LPZ226	1044.9	130.4	1776.9	1210.8	2757.7	3388.5	326.6	3520.3
LPZ227	1078.3	133	1461.7	973.5	7032.1	9452.8	2043.5	4705.3
LPZ228	3961.6	213.5	3373	4050.7	5575.6	10714.4	2428.6	5928.9
LPZ231	3475.2	230	4096.3	3841.1	5009.3	5690.3	959.9	5514.3
LPZ233	2404	218.2	2170.9	1531.4	4362.7	4198.1	673.7	3350.1
LPZ234	1688.3	312.3	1887.6	1486.5	4228.6	4715.6	724.8	3170.1
LPZ235	2661.6	199.9	2422.2	1852.6	3078.9	2886.6	98.2	3143.5
LPZ237	3174.5	324.2	3032.5	2988.2	3931.1	4587.9	314.4	4588.3
LPZ239	4061.3	309.3	3175.1	2932.1	4131.7	3892.6	122.3	5083.5
LPZ240	3799	316	3730.6	3314.6	3379.8	3538.8	212.4	4784.5
LPZ241	2559.2	62.1	2610.4	1794.5	4165.6	3754.4	134.8	2915.1
LPZ242	29360.5	3262.9	35254.6	25196.9	43028.8	31468.2	7308.4	36768.4
LPZ243	3405.3	88.8	3015.7	2683.4	3678.7	2990.6	121	4001.4
LPZ244	4856.9	483.6	4842.2	5235.3	5317.6	5432.1	205.4	5712.9
LPZ246	1274.8	65.9	2301.7	1922.8	4332.2	4628.8	672.1	4232.4
LPZ247	3894	69.8	2522.8	3389.9	4451.4	4937.1	939.3	5522.8
LPZ248	3016.7	268.6	2883.2	3805.2	3791.7	3777.6	487.1	4585.6
LPZ249	5224.1	138.3	3524.5	4091.2	3022.4	3393.2	149.9	4101
LPZ250	1060.6	46.5	1400.9	1246.9	1419.5	1411.2	118.8	2908.4
LPZ251	1336.8	248.5	1354.6	1049.3	657.6	924.3	70.3	2064
LPZ255	3787.8	171.8	4801.8	5076.3	4608.1	4965	340	5636.6
LPZ256	536.6	61.6	865.5	971.6	1130.8	1327.7	82.7	936.9
LPZ257	844.5	112.6	1507.4	1537.8	2337.9	2745.8	341.5	1610.7
LPZ258	2588.5	142.3	3443.1	2902.2	4576	4976.4	1182.9	3619.6
LPZ260	897.7	113.7	1677.9	944.3	1217.6	1286.6	170	2928.2
LPZ261	981.3	132.1	1499.6	743.4	1590.8	1953	67.2	1652.1
LPZ264	4559.3	231.3	4348.5	2856.3	4869.2	5179.7	412.3	4698.3
LPZ265	21063	2793.9	26928.5	12365.5	13816.5	12134.4	691.6	17954.8
LPZ266	1642.4	130	1767.5	1463	1633.8	1410.5	59.4	1444.5
LPZ268	2451	114.2	2803.3	2495.4	3126.5	3433.7	79	4261.3
LPZ269	15670.7	3660.5	35782.4	21720	40375.2	31597.3	2024	35213.6
LPZ270	3541.2	240.8	3803	3132.4	4827.8	5213.6	79.9	5473
LPZ271	5590.7	677.2	5465.4	5197.1	5703.4	5615.2	309.2	5732.7
LPZ272	27369.6	3445.9	35824.6	22832.6	40684.8	27398.4	1732.9	37016
LPZ273	1107.3	46.1	456.7	336.3	1879.3	1654.1	65.4	971.9

TABLE II-continued

LPZ274	3936.2	114.5	3192.3	3024.1	4983.3	4907	293.9	4933.5
LPZ275	2567.2	42.9	1760.4	2091.8	3656.5	3800.5	77	2585.4
LPZ276	560.9	32.9	1075.4	1878.9	1889.9	1766.2	66.8	1294
LPZ277	423.7	34.6	1199.1	1169.8	1376.8	1383.9	91.9	1123.7
LPZ278	323	39.7	937	382.9	770.1	935.2	66	1403.4
LPZ279	965.9	70.7	1907.5	1368.2	1783.7	1603.9	133.2	2438.8
LPZ280	390.7	19.6	175.4	42.3	464.9	631.5	29.9	2074.9
LPZ281	84.3	8.2	0	0	0	0	9.7	0
LPZ282	1849.7	28.4	315.1	34.2	664.3	1097.3	21.5	1229.5
LPZ283	10678.6	329.2	5134.7	5311.1	4772.3	8591.1	226	9633.6
LPZ284	996.1	39.8	236	147.2	2349.5	981.1	26	719.7
LPZ286	563.8	77.1	1031.1	945.9	1347.4	1601	81.2	1303.6
LPZ287	1045.7	123	2057	1475	1730.9	3003.6	149.9	2493.5
LPZ288	1201.7	116.2	1797	1448.8	1648.3	670.4	80.6	3700.4
LPZ289	1922.3	113.3	2515.4	3395.3	3460.7	3369.4	70.8	2183.8
LPZ290	14629.5	3945.8	34659	24047.3	40474.8	27786.2	1348.2	27566.4
LPZ293	4364.8	385.4	4664.2	3170.9	4321.6	4789.8	74.6	5095.8
LPZ294	564.7	171.4	1257.5	705.2	1357.7	1610.2	18.6	2027.6
LPZ295	823.1	97.3	2102.7	1056.2	2899.7	2698.3	39.4	2448.2
LPZ297	5273.4	169.1	5229	5074.4	5727.8	11512.9	423.2	10966.8
LPZ299	1564	161.1	1743.9	1752.3	2764.1	2660.5	63.5	2791.9
LPZ300	3068.3	205.4	2406.8	1881.8	2898.6	2758.4	0.2	2007.2
LPZ301	1979.7	233.1	3207.1	2109.3	4343.5	3713.8	40.4	2690.6
LPZ303	509	32.7	281.3	877.7	893.1	751.5	30.1	1373.8
LPZ304	2531.1	289.3	3809.4	3406.7	3674.8	3517.4	158	2652.7
LPZ306	22632.7	2861.2	34933.8	25435.6	40453.9	30906.9	1505.9	34032.8
LPZ307	2604.4	1395.2	4780.6	6945.3	4419.2	4416.9	232.6	4299.8
LPZ308	1093.9	60.5	2028.1	1751.6	1770.8	1891.9	92.4	3245.8
LPZ309	286.1	26	480.4	378.4	589.6	731.4	38.4	1062.4
LPZ310	2284.1	129.5	1622.7	1091.7	1207.1	3089.4	101.2	3624.9
LPZ311	3309.9	43.6	2782.6	2956.3	2828.8	4446.7	95.8	5593.4
LPZ312	446.3	52.7	1577.7	1221.4	542.2	518	56.1	1952.6
LPZ314	378.6	26.9	333.9	355.8	682.2	701.2	61.7	732
LPZ315	3897.5	115.2	2611.9	3145.8	4296	5240.2	151.3	4499.3
LPZ318	9709.6	767.1	19964.9	15678.3	20611.8	19600.2	475	18079.9
LPZ320	1126.7	82.8	1215	1002.7	1502.5	1555.3	67.5	2964.4
LPZ321	2944.7	85.4	2590.7	2597.6	2550.3	2962.7	72.1	5481.4

Clone	ZE1	ZE2	ZE3	ZE4	ZE5	ZE6	ZE7	ZE8	ZE9.1
LPS001	369.9	369.9	369.9	369.9	369.9	369.9	369.9	369.9	369.9
LPS003	600.3	363.9	0	243.7	1565.3	2624.5	1942.7	242	1892.5
LPS004	522.3	254	0	74.6	907	2638.8	1933.6	274.9	4209.2
LPS006	444.6	161.2	0	174.6	793.6	2651.4	1991.5	206.5	598.8
LPS007	528.9	136.3	0	244.9	1623.3	1202.1	2044.7	245.1	213.9
LPS008	534.5	215	0	281	1231.2	783.4	1760.3	178.5	832.4
LPS010	469	183.6	1.3	240.1	947.7	591.6	2208.3	161.2	482.6
LPS011	468.7	93.3	0	142.3	1544	1021.5	2334	254.6	1223.7
LPS012	511	278	17.7	197.2	2129.6	68.9	1362.7	478.9	960.4
LPS013	478.2	407.1	192.1	235.6	2470.6	9	1163.9	885.7	1109.4
LPS014	579.7	369.1	0	272.7	2799.6	1525.7	2222.4	606.9	2638.6
LPS015	419.7	254	0	2380.7	7188.1	4998.4	16519.6	5245.1	15550.4
LPS019	1068.4	279.6	0	396.2	3848.5	3074	3866.9	959.1	3664.7
LPS020	314.2	109.1	0	102.7	2036	234.4	1504.2	319.6	1053.2
LPS023	364.9	104.2	0	100.7	1151.8	0	1253	175.5	570.5
LPS024	804.7	213.8	0	346.3	3248.5	2523	2722.6	915	1987.4
LPS025	1374.7	407.8	0	857.1	4731.2	2584.2	4119	1138.4	2458.4
LPS026	337.6	86.1	0	100.2	1242	0	1052.9	242.9	988.9
LPS027	440.5	182.5	0	118.5	1318	691.2	1274.1	226.1	385
LPS028	369.5	166.2	0	168.7	2587.7	2597.8	4035.5	565.9	1883.1
LPS029	323.4	141.9	0	165.3	2524.3	2147.2	3031.3	567	2263.9
LPS030	362.3	226.5	0	169.6	1528.2	422.9	1236.7	239.2	1049.1
LPS031	591	536.7	4.9	383.6	1768.3	850.4	1013.3	399.8	781.4
LPS032	443.9	327.3	0	328.1	3200.9	1880.1	1832.8	265.6	1391.6
LPS036	1093	781.8	24.5	680.8	3911.3	3750.9	3746.7	661.8	3856.4
LPS037	501.6	180.4	0	200.9	2664	2369.8	1960.5	339.9	2892.9
LPS038	1180.1	471	155.9	1679.7	4392.3	2103.5	3019.9	800.3	2819
LPS040	398.8	108.6	0	103.9	1030.7	195.9	1566.1	144.4	682.1
LPS041	384	153.8	0	149.7	989.2	1257.5	2235.4	143.3	1228.4
LPS042	1381.9	951.7	44.9	716.1	3682.1	2755.7	4011.7	508.5	2963.4
LPS043	1211.6	704.8	74	613.6	3494.4	2435.3	3362.1	391.4	1544.7
LPS044	361.3	100.2	0	142.1	2244.4	3031.8	2653.5	393.4	1620.1
LPS045	285.7	75.2	0	64.4	856.5	223.5	1616.1	216.8	609.7
LPS046	325.8	217.2	0	70.2	1758.6	0	1280.9	284.9	1115.5
LPS047	2041.3	1347.8	768.4	1080.5	4169.9	3927.9	4263.5	1831.6	4804.9
LPS050	3226.4	3356.4	6064.5	3347.5	9841.4	3046	5362.2	2924.8	5821.2
LPS051	377.1	96.4	0	156.8	2452.6	2286.5	3035	396	2238.1
LPS052	330.1	80.1	0	162.6	2418.1	0	2097	352.5	1677.3
LPS053	402.6	160.1	0	146.3	2249.5	56.9	1986.1	464.3	1349.6

TABLE II-continued

LPS054	497.4	147.5	0	184	2188.4	379.1	1976.1	308.6	1558.9
LPS055	1168.2	645.7	0	354.9	3901.1	1476.5	2607.5	774.8	3026.1
LPS056	1549.5	1243.3	37.9	752.6	4770.9	3403.7	4086.8	1204.2	4958.4
LPS057	387.5	154.3	0	262.7	2612.2	502.6	2317.5	365.1	1418.8
LPS058	671.2	198.9	0	434.8	4189.9	2258.6	3366.3	586.3	2190.5
LPS059	726.2	207.5	0	304.6	2974.8	2054.3	2712.8	395.1	1331.6
LPS060	534.2	215.8	0	221.7	2896.9	718.3	2693.3	477	2474.9
LPS061	530.8	369.4	0	204.3	1801.1	1286.4	1533.6	298.7	1327.2
LPS062	407.4	305.2	0	226.4	1509	0	1413.1	212.5	954.6
LPS063	619.4	280.8	0	282	3987.4	1805	2589.9	642.1	1650.4
LPS064	3689.2	4982.4	10201	3080.3	8359.8	3622.3	8304.6	2997	13781.1
LPS065	466.4	189.7	117.3	817.1	4336.3	2332.6	4393.4	1092	3866.8
LPS066	269.5	104.6	0	131.4	1006.2	76.7	1834.6	185.9	668.5
LPS067	426.4	179.7	49.3	341.3	4153	4077.7	5101.3	1195.9	3894.1
LPS069	367.8	136.7	0	128	1456.6	0	2685.6	308.7	1234.3
LPS070	438.5	137.3	0.4	111.6	1932.5	25	3005.3	210.4	721.5
LPS071	283.9	83.2	8.5	109.2	1831.5	0	3634.2	302.8	708.3
LPS072	301	147.2	5.7	132.9	1600.8	592.3	3051.5	331.5	1173.5
LPS073	692.1	485	251.5	497.9	4205.3	2827.4	3777.9	740.1	3882
LPS074	36280.3	66359.2	63362.2	44047.1	47176.9	20938.9	64534.5	33666.4	78457.8
LPS075	3204.8	1250.6	650.9	1033.7	4976.3	4377.1	4632.6	1617.1	5570.9
LPS076	434.7	127.9	0	204.7	1731.3	419.1	2737.8	298.8	2175.1
LPS077	416.6	107.6	0	327.2	3360.7	1950.5	4020.1	609.1	3713.9
LPS078	5164.5	1194.3	906.3	6556.7	20779.8	7364.3	28847	8680	22339.1
LPS079	1317	501.9	304.2	893.4	5047.6	3196.6	4887.5	1058.8	4992.1
LPS080	27721.4	56038.2	70896.6	26826.4	43426.4	20557.3	47819.2	16935.5	68145.5
LPS081	36397.3	66337.3	48195.9	41685.3	46187.5	20628	66138.1	31620	78253.7
LPS083	844.6	534.2	123.6	305.3	3724.2	1699.7	2524.6	583.8	3266.4
LPS084	665	249.4	0	334.5	2570.6	1491.7	2893.2	342.8	2061.7
LPS086	456.6	155.8	0	165.1	1962.7	754.5	1931	130.2	2176.5
LPS087	967.5	450.7	17.2	633	4238	3720.3	5373.9	1754.7	19094.1
LPS088	468.4	276.1	0	151.1	1109.4	0	1779.7	302.8	2497.2
LPS089	329.2	316.9	0	133.6	988.7	0	1619.6	320.7	1616.9
LPS090	478.9	272.3	0	218	4486.4	2182.3	2923.1	584.6	2640.7
LPS091	385.7	177.9	0	290.7	2923.3	2008.6	2453.2	441.5	2246.6
LPS092	396.3	164	0	345.2	2249.1	1219.1	2906.7	413.9	1589.3
LPS093	308.3	164.5	24	98.7	262.3	427.8	2140	175.4	661.4
LPS094	331.6	179	54.2	146.4	773.3	948.2	1729.1	116	1030.7
LPS095	363.7	157.7	46.3	142.5	967.7	341.4	2639.7	199.3	1055.4
LPS096	266.9	90.6	0	59.3	676.5	0	2616.2	136.5	215.6
LPZ001	270.9	49.7	21.1	121.2	1958.2	496.8	4495.7	325.6	557.7
LPZ002	491.7	231.8	157.9	345.8	1929.4	1183.4	3243.9	305.5	932.6
LPZ003	632.6	407.2	342.3	343.5	2630.6	2108.3	3212.8	423	4663
LPZ004	2034.4	2260.7	1487.4	1442.5	5730.7	2135.4	5424.1	1804.4	5786.1
LPZ005	6301.3	4683.6	2801	10127.5	31972.9	7747.5	51335.5	17767	52067.8
LPZ006	471.7	131.2	0	179.4	1964.1	1552.2	2977.9	333.5	2954.9
LPZ007	584.6	383.7	69.3	294.3	1424.1	531	2664.9	265	3021.7
LPZ008	325.4	87.5	14.4	176.8	1966.6	1588.5	2420.1	199.5	3481.2
LPZ009	451.3	281.6	143.4	362.3	3149.2	4280.4	3006.5	357.5	4395.9
LPZ010	1324.5	1442.8	621.8	931.8	4310.4	3238.7	3926.9	617.4	4912.5
LPZ011	1740.9	2073.5	1436.2	1075.8	4631.4	5232.7	4563.3	1080.6	5456.6
LPZ012	424.4	217.8	50.1	271.8	2286.7	713.5	1791.4	390.6	3209.9
LPZ013	395.4	123.8	33.1	181.1	3456.8	2121	2898.4	428.9	2673.3
LPZ015	490.7	210.7	60.8	130.8	2889.2	330.5	2123.4	230.2	2680.6
LPZ016	2411.9	710.9	346.5	1201.2	6897.9	4057.6	13340.1	3246.1	16664.2
LPZ017	635	257.4	36.2	247.2	2797.3	1219.1	3508	558.7	3953.8
LPZ018	1405.4	474.9	214.9	3188.7	8143.7	4992.8	12908.9	4208.2	14318.9
LPZ019	3487	975.9	698.4	8916.5	23680.5	15131	31656.3	14191	45343.3
LPZ020	251.9	195.6	0	40.9	1448.5	860.4	1113	305.5	971.2
LPZ022	250.1	112.4	0	133	2085.9	1282.5	2538.5	532	613.2
LPZ023	355.5	122.6	22.9	47.8	224	879.4	1419.1	132.3	605.4
LPZ024	366.5	108.9	45.7	94.8	225.3	723.1	1276.8	81	319.5
LPZ025	705.4	278.6	202.1	716.7	5145.5	4563.4	7215.5	1581.9	4195.8
LPZ026	268	100.6	9	92.1	1164.5	750.4	3973.6	275.5	642.3
LPZ028	386	174.2	96.8	374.9	4188.4	2733.8	7024.6	1186.8	2375.6
LPZ029	221.9	86.8	0	47.8	225.3	264.4	2172	162.4	957
LPZ030	319	166	67.6	146.9	801.6	1385.4	2283.4	145.8	1189.4
LPZ031	2010.6	881.7	538.1	754.3	4625.8	3395	4051.7	1327.9	5202.1
LPZ032	36097.5	35972.1	13659.1	19975.4	45544.5	20035.8	63759.8	31117.4	78268
LPZ033	1813.8	433.6	243.7	1171	7402.4	2278.7	10670.5	2204	5643.8
LPZ034	332.6	97	34.6	181	1097.2	0	2704.1	262.6	3481.4
LPZ035	248	60	0	71.4	1188.8	0	1332.5	153.6	3028.4
LPZ037	375.8	133.8	0	114.6	3024.3	909.1	2350.6	248.2	3546.8
LPZ038	577.7	237	44.3	370.7	4484.6	3572.5	4266	907.9	4571.4
LPZ039	965.6	406.7	361.2	537.9	4020	2304.1	4269.9	816	3717.5
LPZ040	399.9	127.4	0	88.3	1200.5	365	2123.2	244.3	1955.4
LPZ041	318.4	105.1	0	136.6	856.3	716.6	1528.5	245.6	1538.5
LPZ042	289.3	77.6	0.9	189.5	441.5	365.4	1007.7	239.2	1212
LPZ043	417.3	166.7	57.4	158.2	1197.2	1617.9	793.5	569.1	2018.7

TABLE II-continued

LPZ045	754.8	310.3	152	691.5	4810.4	3305.3	4043.7	1476.3	3925.7
LPZ047	270.5	155.4	53.1	39.1	2165.6	579.6	980.9	361.7	1036.3
LPZ049	809.6	381.9	0	461.4	4406.4	2277.4	4764.6	2257.8	5528
LPZ051	333.1	121.5	0	56.6	1597.8	1677.8	891	270.7	1134.6
LPZ053	271	119.7	0	16	1662.4	2447.8	1202.4	201.1	827.1
LPZ054	345.4	131	61.7	79	1181.1	2238.5	1426.5	156.5	627.5
LPZ055	291	78.1	102.9	63.5	551.3	2343.8	1433.5	193.6	814.2
LPZ056	364.6	167.9	83.6	130.3	1816.9	2580.4	2589.4	343	1579.8
LPZ057	250	76	0	11.9	426	457.6	2589.6	113.4	709.8
LPZ058	231.1	40.8	6.2	44.4	454.7	163.4	3403.4	208.5	1300.4
LPZ059	239.2	78.6	0	15.7	189.7	267	3272.7	141	1439.2
LPZ060	235.1	26.7	29.4	35.6	524.8	1238.2	2231.2	182.5	1908.8
LPZ061	402.1	268.4	141.6	254.6	1694.1	3088	2343.5	557.3	4157.7
LPZ062	727.7	146.8	0	203.3	2873.3	2418.9	3109.6	926.6	5812
LPZ063	316.7	108.2	25	190	1837.3	1025.1	2727.2	421.8	4195.9
LPZ065	512.5	59.9	94.9	583.5	5694.4	3741.6	5366	1221.6	3911
LPZ066	622.2	66.8	23.8	405.6	6932.1	3089.5	4804.9	642.2	4079.9
LPZ067	883.7	218.7	0	358.7	4518.2	2342.9	5200.8	1318.4	5539.6
LPZ069	335.6	100.2	0	46.8	0	0.7	1736.5	255.4	2910.4
LPZ070	422.6	143.3	49.6	168.8	1231.5	1170.6	2432.2	262.7	2122.5
LPZ071	356	71.9	0	299.7	2303.6	1909.8	2575.9	447	2827.6
LPZ072	206.5	32.6	0	71.7	0	0	1362	189.6	907
LPZ073	374.2	129.6	32.1	125.8	307.4	691.8	1617.6	282.4	1306.9
LPZ074	434.7	86.5	0	76.6	1671.1	0	1112.5	232.7	663.5
LPZ075	298.5	173.5	0	53.5	4083.2	0	1143.9	113.7	335.1
LPZ076	209.9	83.1	7.2	7.4	2185.9	0	490.5	226.6	362.9
LPZ077	813.4	558.3	0	339.1	3733.4	4279.8	1115.9	671.7	4136.8
LPZ078	532	349.8	0	265.8	4460.1	3290.7	2776.8	686.3	3283.3
LPZ079	347.8	183.6	11.6	53.3	2115.4	1191.7	1451.2	160.5	1233.2
LPZ080	948.1	264.9	178	455.1	4633.9	2869.1	4230.5	1378.5	5566.5
LPZ081	313.7	96.1	100.2	59.7	1161.6	1470.2	1119.7	98.5	710.9
LPZ082	260.9	120.3	18.4	68.3	1734.5	1430.6	1581.6	160.1	379.4
LPZ083	284.9	134.6	12.6	7.8	1067	906.1	1482.7	107.2	790.5
LPZ084	1493.3	437.1	0	788	4497.3	4608.3	5078.9	2267.8	5087.7
LPZ085	468.1	139.4	0	62.1	1618.8	1355.9	4314.9	340.5	2421.5
LPZ086	601.3	91.6	11.9	332.9	3540.3	3354.6	6675.2	781.2	5545
LPZ089	457.1	124.1	26.2	267.7	2378.1	3364.6	3390.2	448.7	2930.7
LPZ090	436.6	50.7	0	149.1	3135.3	2087.8	3090.4	483.8	3408.1
LPZ091	350.2	91	96.2	99.2	1524.3	1976.3	3215	315.9	4532.8
LPZ092	387.6	33.6	0	114.4	2386.7	2600.9	2845.7	274.6	2036.7
LPZ093	195.6	25.8	0	27.1	2343.1	321.7	2875.2	252.7	1428.2
LPZ094	274.8	42.8	0	35.2	886.9	0	2502	152.6	1571
LPZ095	288.6	91.5	0	14.1	3.5	0	2317.2	144.4	1427.4
LPZ096	475.4	138.7	13.1	199.2	1690.8	1415.2	3939.2	207.2	1889.7
LPZ099	428.1	73.8	0	185	2531.8	2596.6	3925.9	399.8	1967.5
LPZ100	474.3	131.1	24.6	266.6	2710.6	2276.7	3358.6	503.5	2245.1
LPZ101	492.1	101	81.9	233	2341.4	2076.1	2199.9	423.1	2022.4
LPZ102	477.3	133.2	0	167	3722.9	1604.4	2432.1	386.5	1199.8
LPZ103	353.5	90.7	0	108.9	4756.8	214.4	1447.5	203.9	760.7
LPZ106	534	199.4	58.6	117.6	3052.4	1259.2	1610	277.6	1224.3
LPZ107	29718.3	56194.4	31132.5	35651.5	44972.5	20589.6	38396.3	32828.7	75965.1
LPZ108	852.4	433.1	161.4	417.4	4354.8	2259.1	3536.9	1168.5	3161.8
LPZ109	554.2	248.6	83.8	254.6	3303.4	2521.1	1972.8	608.5	2858.5
LPZ110	614	203.3	166.1	182.1	3236.7	2792.6	2764.1	455.5	3139.2
LPZ111	349.5	167.7	77.4	82.9	1407	1386.1	1469	200.9	1397.5
LPZ112	497.3	279.2	65.3	242.6	3553.5	2504.1	2454.6	328.3	2182.2
LPZ114	890.2	346.7	0	399.3	4520	3367.9	2902.7	1229.6	3474.1
LPZ115	24782.8	12016.1	1401.9	12188	32718.2	17087	38203.9	17191.1	25318.5
LPZ116	1388.1	392.7	0	884.6	8895.4	3131.2	15554.1	2195.7	5401.6
LPZ117	6228.4	4810.2	389.7	1298.8	4199	2671	5473.5	1488.2	3911
LPZ118	424.5	267.3	39.9	196.2	2507.4	2210.1	2856.3	370.3	2640.4
LPZ119	295.1	183.4	0	59.8	2443.3	1153.2	2040	158.7	1132.1
LPZ120	213.5	88.4	49.2	185.9	1336.6	1390.4	1604.5	186.7	1360.8
LPZ122	317.6	120.3	0	92.1	1390.2	2045.1	1701.2	112.5	1307.5
LPZ124	346.6	173.2	38.9	119.4	2097.9	543.9	2679.2	221	1941.7
LPZ126	436.1	185.4	0	142	1762.2	0	2164	283.2	2343.6
LPZ127	455.7	208.6	0.1	109.8	1091.7	1925.5	3143.4	345.4	2565.8
LPZ128	421	602.3	25.1	651.1	4496.3	2712.3	5456.8	1177.7	3875.7
LPZ131	287.1	401.2	0	58	1931.2	422.4	3510.2	232.2	1275.8
LPZ133	377.8	399.9	141.9	139.5	2396.5	1989.9	4287.5	388.9	1119.6
LPZ136	455.2	191.7	103.3	239.9	2289.7	1775	2586.1	322.4	1429.8
LPZ137	398.1	123.1	0	214.7	2480.2	1118.7	2138.5	411.3	1935.9
LPZ138	1987.8	1102.2	11.9	1112.7	4785.6	4242.8	3044.7	1298.3	2786.7
LPZ140	401.4	205.9	115	316.7	2737.2	1950.6	1491.6	414.2	2031.4
LPZ141	917	621.2	0	726	4938.4	3889.9	3237.4	1109	4165.8
LPZ143	4702.9	1483.9	774.8	6791.2	20187.4	6913.4	23175.5	10795.1	26322.7
LPZ144	529.7	392.6	25.7	303.5	2644.9	1902.4	2380.9	486	2422.7
LPZ145	410.2	206.5	25.4	152.3	1618	2219.1	2012.8	357.8	2494.3
LPZ146	294.2	152.3	0	125.3	1063.5	1142.1	1129	215.1	1927.1

TABLE II-continued

LPZ147	366.5	238	0	246.5	2120.4	956.1	1343.4	260.2	1539.3
LPZ148	390.6	212.9	0	170	2107.1	2195.4	1832.6	1240.9	3839.8
LPZ149	1872.8	1139.7	218.5	1748	6204.2	1641.3	5144.7	3526.5	5193.6
LPZ150	1958.1	1284.1	645.6	10615.2	29419.9	2976.7	52052.2	21478.7	41125.9
LPZ151	3477.3	1936.4	155.4	1423.9	5253.1	1925.1	5434.9	2248.3	5180.5
LPZ152	963.2	481.9	42.2	658.9	4770.8	3607.7	4661.8	1003	4661.9
LPZ153	13685.9	27883.7	11205.9	13827.1	24872.9	15412	26204.7	12163.3	41713.9
LPZ154	621.9	470.5	45.6	381.1	2965	2584.3	2802.2	416.8	2738.4
LPZ155	2004.5	1513.1	388.4	1358.9	4265.3	4159.3	4386.4	1022.6	4543.9
LPZ157	2978.4	1332.8	407.8	1400.6	4650.6	3692.3	4760.8	1195.9	5002.5
LPZ158	12352.4	18933.2	12155.7	9376.4	23120	15280.6	18384	10293.8	50995.4
LPZ162	3778.2	4069.3	426.4	2285.5	6458.4	3004.6	5794.3	4161.4	13171.9
LPZ165	1181	805.1	0	756.4	4641.9	2702.4	5464.6	1470	4822.6
LPZ166	4624.9	5016.4	0	2508.8	9907.8	1939.3	5655.3	2999.9	5667.6
LPZ167	3339	1655.9	319.8	1101.8	4807	4980	4678.8	1968.2	4248.1
LPZ169	787.5	556.1	226.4	461.9	2830.2	2225.4	3549.7	684.4	3249
LPZ170	851.1	501.5	0	589.6	4405.2	4440.6	4652.4	1622.7	4556.9
LPZ171	1325.6	612.2	0	697.6	3647.5	3148.7	3446.8	1053.8	4043.4
LPZ172	748.6	490.4	0	802.4	3953.2	2939.1	3550.9	848.3	3809.5
LPZ173	4460.6	3415.7	1050.1	5769.8	16078.4	6658.8	16861.6	8623.4	21007.1
LPZ174	501.9	308.6	36.2	358.6	3054.1	1731.2	1954.9	862.9	2773.9
LPZ175	1476.5	1057.1	181.6	836.9	3731.4	3120.9	3879.4	755.9	3687.2
LPZ177	302.3	228.3	18.6	107.1	753.6	1430.4	941	165.4	1411.2
LPZ179	616.8	314.9	8	379.4	4544.7	2954.4	3425.3	1361.5	5310.3
LPZ181	1103	430.7	0	671.3	4917.1	3821.3	4976.3	2646.1	5785.8
LPZ182	992.8	435.1	0	468.1	3930.1	4177.6	3287.5	909.9	4820.2
LPZ186	2455.7	1428.7	760	2414.4	9679	4431.1	5537.9	3859.3	5921.7
LPZ189	40770.3	68311.4	75133.7	45673	47303.1	21072.6	66542.7	34849.1	78485.4
LPZ194	612.8	572.1	155.6	376.3	3673.5	2240.2	3365.2	469.5	3608.6
LPZ195	676.9	346.6	32.5	459.9	4278.1	4622.4	4442	1006.8	4754.3
LPZ196	2923.1	1787.1	448.6	1537.1	4490.3	3684	4875.6	1426.9	4447.8
LPZ197	592.3	177.5	343.1	629.4	5825.4	3639.7	4308.7	649.9	2838.2
LPZ198	801.7	295	8.2	511.1	4384	3156.4	4823.8	1125.6	3947.2
LPZ199	402.5	165.1	62.7	265.9	2158.3	2363.7	3531.7	423	2360.1
LPZ201	1338.5	361.2	209.6	1053.7	4997.8	4565.6	5107.6	2350.9	5882.2
LPZ202	8178.9	2795.3	2359.9	12950.9	39890.9	20247.9	62085.4	31826.4	78541.6
LPZ203	1983.5	1083.8	1146.8	2044.1	9173.9	2174.8	11135.5	4073.8	19571.3
LPZ204	38154.8	66241.1	88440.7	45372.1	47166	21054.3	65826.6	33875.6	78581.7
LPZ205	1079.5	521.7	589.1	758.4	4742.5	3837.7	5220.2	1453.2	4888.6
LPZ206	947.6	700.1	505.1	697.8	4089.6	2774.1	5242.9	1190.3	4578.7
LPZ207	39899.6	60813.3	95637.5	45997	47123.6	21073.2	63996.4	35149.4	73080.5
LPZ208	27268.6	27230.4	39428.3	29579	40216.5	20480.2	42465.8	26526.9	76872.4
LPZ210	683.8	538	429.6	439.8	2402.5	3285.4	2419.1	636	3965.6
LPZ211	603.1	530.3	87.2	434.6	3653.3	2234.5	1744.1	359.8	1644.7
LPZ212	1018.4	580.7	155.2	1734.1	9212.3	2338.9	5061.9	2257.3	4303.3
LPZ213	465.6	327.1	33.1	296.6	3012.3	2419.4	2198.4	570.9	2013.9
LPZ214	245.6	267.4	0	160.5	912.5	756.5	880.7	133.9	936.8
LPZ215	981.1	492.8	52.3	828.3	5390.6	4771.4	4868.1	2893.1	15622.6
LPZ216	9410.5	3834.8	1843.2	14492.9	43137.1	21097.9	63778.6	34830.7	78538.8
LPZ217	31119.9	47126.3	30689.1	28515.4	38695.3	19884.5	37913.9	21282.9	69590.2
LPZ219	1300.2	886.5	475.3	946.3	4898.3	4361.6	3705.4	1784.6	5810
LPZ220	5695.5	7233.6	9375	4579.9	6540.8	4340.1	5612.6	2993.6	5852.3
LPZ221	242.6	209.5	0	186.3	2553.4	2132.5	1632.9	258.2	3202.9
LPZ222	186.9	130.5	0	163.4	2138.4	1386.3	1855.4	223.3	2407.6
LPZ223	289.9	168.4	0	164	2019	1582.7	2374.4	250.3	2309.2
LPZ224	308.3	114.3	20.5	333.9	2467.7	2535.2	2722.9	518.9	3054.9
LPZ225	5540.8	1287.2	919.3	7087.6	18926.6	9277.7	20292.9	8705.5	19974.7
LPZ226	179.1	111	9	136.8	1049.8	2071.1	3332.8	463.4	2517.8
LPZ227	243.5	136.2	0	341.4	2502.5	2597.6	4869.5	3226.2	16356.7
LPZ228	470	249.6	0	349.2	4062.6	3388.6	5688.3	2586.2	15112.1
LPZ231	480.4	296.3	87.4	326.6	3832.4	2343.1	5557.3	1542.5	5679.2
LPZ233	468.6	332.9	161.7	350.3	2519.3	1967.1	5201.8	996.1	4833.8
LPZ234	525.8	368.6	287.8	380.3	1626.6	1285.8	4231.8	1235	5329.5
LPZ235	310.7	233.3	0	370.2	1746.3	1474.1	4135.8	541.1	3382.9
LPZ237	683.5	468.8	487.2	506.9	3683.2	2108.7	3966.8	1369	5254.5
LPZ239	546	192.6	339.2	331.5	2584.8	2384.8	3215.7	754.4	4041.1
LPZ240	353.7	280.8	163.9	274.8	2281.8	1696.4	2345.8	319.2	2180.8
LPZ241	283.3	260.2	0	206.4	2481.1	1787.8	775.1	426	1729.3
LPZ242	7478.4	2664.4	1039.1	7024.1	22393.3	11120.5	20928.9	8581.6	22951.9
LPZ243	242.4	167.1	0	157.2	2175.8	182.4	806.9	237.7	977.2
LPZ244	350.3	206.1	0	409.4	4522.7	3997.1	4486.3	1022.8	3387.1
LPZ246	260.9	200.9	0	251.8	1930.9	1335.1	995.1	1033.7	4712.9
LPZ247	438.3	274.4	0	341.4	2994	2325.3	2926.7	1508.7	5494.3
LPZ248	748.4	714.1	291.3	878.4	3814.2	2737.7	3489	1155.1	4689.5
LPZ249	373.3	375.6	0	613.1	4798.1	2088	3560.8	433.5	2486.3
LPZ250	159.5	201.7	0	317.6	2037.8	2085.9	1721.8	220.5	2051.7
LPZ251	141.7	157.9	0	178.9	1377.4	1723.8	1136.8	91	1271.1
LPZ255	220.8	176.1	0	646.5	4160.8	2725.5	5110.3	1217.2	5217.7
LPZ256	94.6	101.7	0	149.5	821	812.6	1989.5	65.4	432.2

TABLE II-continued

LPZ257	147.9	118.4	0	135.1	1206.9	1208.1	2197.2	207.9	745.8
LPZ258	168.3	124	0	174.7	2264	2172.4	2672.8	532.8	2245.2
LPZ260	213.5	172.9	0	141.3	1172	2974.6	4118.3	232.4	1057.4
LPZ261	147.2	78.5	0	126.6	1212.5	2349.9	4604.9	139.4	741.8
LPZ264	318.3	174.1	0	201.7	3104.4	2387.6	5505.8	582.7	3775.1
LPZ265	1566.8	449.9	129.7	646	4992.3	3477.7	5635.5	988.7	4307.2
LPZ266	92.8	287.2	0	132.5	931.4	0	4689	190	726.3
LPZ268	171.3	217.2	0	206.8	2142	2135.8	5156.3	296.8	1912
LPZ269	1530.1	571.5	419.3	2333.1	11130.7	4947.4	13881.5	5155.2	5755.6
LPZ270	162.3	291.4	0	450.4	3822	3736.4	4342.8	978.4	2987
LPZ271	454.6	266.6	45.9	381.8	3194.7	2859.7	3598.7	1277.5	4054
LPZ272	2943.2	763.9	613.2	1451.3	7894.9	2900.8	5222.6	3222.4	16317.5
LPZ273	215.5	178.7	0	112.2	1288.3	908.3	145.5	182.5	544.8
LPZ274	271.5	189.3	0	322.8	3311.7	1141.5	1301.4	620.8	3182.2
LPZ275	174.5	152.8	0	99.6	1052.3	0	0	109.3	887.1
LPZ276	146.8	139	0	129.4	1165.3	123.5	505.4	82.6	461.9
LPZ277	201.8	137.5	1.8	57.1	761.5	931.9	497.5	106.1	1427.3
LPZ278	177.9	152	0	76.6	588.2	1424	311.2	107.3	1178.8
LPZ279	183.3	179.3	0	304.9	2458	1032	524.7	276	1530.9
LPZ280	142.1	125.5	0	125.6	1116.5	623.5	1147.9	125.4	770.5
LPZ281	18	109.8	0	58.9	563.4	850.5	564.6	11.5	317.8
LPZ282	54.3	164.1	48	95.5	1493.6	1874.9	1033.3	54.7	844
LPZ283	1607.8	392.6	48.4	1220	6358.1	2922.6	5552.8	1970.3	5032.3
LPZ284	42.5	119.4	0.3	48	804	748.4	1365.8	66.6	0
LPZ286	34.3	164.5	0	74.8	973.6	1463.4	1205.7	81.2	329.3
LPZ287	118.8	186.4	0	116.4	1573.7	1568.6	2124	252.9	884.4
LPZ288	103.4	162.8	0	78.3	1328.1	2890.4	4192.3	196.9	598.1
LPZ289	137.1	87	0	113.6	2096	2101	5147.9	332.3	913.7
LPZ290	1598	425.5	186	1782.8	10543.9	4598.5	16706.4	3923.8	5648.6
LPZ293	155.8	225.7	0	129.9	3228.2	2291.5	4891.2	316.9	2001
LPZ294	65.5	180.6	0	66.6	2237.5	527.7	4397.4	127.5	688.2
LPZ295	119.9	258.8	0	149.7	1964.6	560.6	5062.1	141.5	897.3
LPZ297	333.9	277.6	59.4	830	5667.2	3950.7	5680.5	1452.6	3614
LPZ299	102.6	225	12.2	268.1	734.7	898.2	4025.5	371.2	913
LPZ300	231	271.7	97.1	42.6	113.2	1713.7	3264.5	4295.2	631.1
LPZ301	272.7	378.2	155.6	97.2	77.2	2110.4	1733.8	485.6	1392.8
LPZ303	145.6	184.3	641.8	52.8	1562.5	1072.8	365	55.5	358.3
LPZ304	422.5	346.5	108.2	350.8	3262.7	2215	1102.8	264.1	1534.7
LPZ306	2207.6	484.7	609	3182.2	9671.4	3639.8	17157.3	3556.4	15015.7
LPZ307	1761.1	1119.4	454.7	846.1	4114.9	2673.3	4082.5	554.8	2983.5
LPZ308	153.5	213.5	85.5	113.3	1369.9	1433.3	133.8	123.2	1146
LPZ309	132	192	14.3	49.2	1137.6	1626.7	126.9	85.1	805.1
LPZ310	325.9	353.6	311.3	253.1	4210.4	2703.3	1846.5	513.3	3102.9
LPZ311	176.9	217.7	72.3	245	3652.2	4352.6	4175.7	734.7	4625.7
LPZ312	70.4	177.2	139.4	53.2	2094.2	1461.1	945.5	57	274
LPZ314	247.5	221.2	217.2	66.9	1767	753.8	872.4	93.1	751.2
LPZ315	167.6	220.4	322.5	172.9	3442.4	1985.7	2505.1	698.5	3667.7
LPZ318	912.5	297.8	441.9	957.6	7473.1	2682.6	6826.4	2471.8	5148.9
LPZ320	7.3	212.8	154.8	55.8	1682.1	1548.5	1038.5	111.1	822.5
LPZ321	199	259.6	157.2	96.8	2588.8	2465.4	3436.8	409.2	3989

Clone	ZE9.2	ZE9.3	ZE9.4	ZE9.5	ZE9.6	ZE9.7	ZE9.8	ZE9.9	ZE9.10
LPS001	369.9	656.8	1322	4095.5	4733.4	7892.2	3248.2	5064.2	6260.9
LPS003	442.5	392.9	262.1	648.7	2035.7	570.6	4524.4	1332.8	543.9
LPS004	811.4	552.2	515.2	1694.9	2438.2	425.1	1218.8	714.3	86.8
LPS006	271	141.2	200.2	0	662.1	1245.1	261.5	1282.6	405.7
LPS007	212.1	91.8	139	47.7	243.4	0	929.2	568	267.1
LPS008	197.6	196.8	224.7	0	235.1	2144.5	1034.5	985.2	307.3
LPS010	152.7	133.4	253.8	241	299.5	1667.7	242.1	1218.8	1170
LPS011	186	136.1	257.9	816.5	257.4	2372.2	77.7	1377.7	1346.8
LPS012	317.2	238.4	236.4	817.5	1316.7	1626.1	0	1324.1	564.7
LPS013	349.5	403.6	412.9	1840	1582.6	2769.8	215.4	1196	1328.8
LPS014	511.4	1574.1	257.3	4169.4	5035.7	4543.5	1016.4	3744.8	3779.2
LPS015	2495.9	3076.7	1720.8	7899.3	3640.5	7103	1228.1	5376.7	11989
LPS019	1028.2	604.5	239.7	3074	2189.3	2161.1	1239.9	2955	2426.7
LPS020	324.1	222.9	120.5	1214.3	1056.8	676.2	872.7	916.8	1058.1
LPS023	160.9	116.3	50.3	623.9	1984.1	0	640.7	349.7	694.3
LPS024	359.3	324.3	198.9	1596	2789.8	1253.1	1212.2	2644.1	3158.3
LPS025	614.7	616.8	493.6	3452.4	3736.3	3726.5	1796.1	4133.4	5569.5
LPS026	153.7	494.7	0	3053.4	3077.5	2157.2	806.2	3886.5	2133.1
LPS027	132.2	267.1	0	1309.2	2323.4	1330.2	1501.6	1931.3	1355.1
LPS028	214.3	446.5	155.7	2472.5	3336.1	2467.9	2987.9	4507.5	3530.8
LPS029	202.7	384.3	223	2040.4	2060.5	2600.8	7214.8	4150	3867.7
LPS030	113.5	132.5	0	515.6	2793.9	110	2158.7	2684.7	1237
LPS031	168.7	123.5	11	557.6	3086	812.5	6212.6	2534.1	3290.9
LPS032	145.2	160.9	1.7	650.5	2144.2	1070.8	1474.2	2819	3561.4
LPS036	582.6	616.4	200.9	2224.2	2656.4	1723.6	3073.1	1866.1	2955.4
LPS037	502.6	620.4	219	1626.6	3359.2	2705.7	2125.3	2456.9	2004.1

TABLE II-continued

LPS038	962.6	216.5	375.7	0	1256.5	930.9	1492.9	1578.3	1406.9
LPS040	228.9	86.1	158.6	0	256.8	0	245.1	758.3	1.7
LPS041	222.7	149.2	123.3	0	252.4	0	965.1	1065.9	553.4
LPS042	447	661.1	489.9	1672.8	2520.7	492	1046.8	2834.7	1940
LPS043	333.7	264.6	407.3	656.8	1046.4	546.5	1412.3	1097.9	948.4
LPS044	249.8	277.8	652	1327.3	907.5	1110.5	1892.3	1353.4	1674.8
LPS045	250.7	107.2	177.9	302.6	231.9	944.7	1881.7	0	485.4
LPS046	232.4	285.6	224.5	1302.1	1872.6	1104.6	2610.7	1128	1744.2
LPS047	2649.2	6969.7	2792.6	14436.1	10141	5428.8	4057.3	2999.2	13647.7
LPS050	2428	7502	3442.1	12204.8	7385.4	9850.6	3395	8052.4	14726
LPS051	478.2	219.7	175.1	1861	2222.1	1876.9	1922.5	800.9	2052.9
LPS052	328.2	196.2	138.3	984.6	1458.3	1324.4	1585	1112.9	1726
LPS053	264.2	111	0	1370.2	1524.9	1548	2692.1	2941.5	3096.1
LPS054	285.4	231.1	8.5	1370.4	2138	1273.8	2930.8	2762.2	2604.2
LPS055	1192.2	1118.8	180.5	5840.8	4203.1	3690.8	1865.1	3205.9	4824.3
LPS056	1541.6	2959.9	1354	9519.2	8084	6331.3	1820.6	5902.8	11668.9
LPS057	214.5	406.9	0	2028.8	2744.4	756.5	2136.1	1844.8	2454.6
LPS058	277.4	244.5	70.8	1623.9	1826.1	1626.5	2708	2514.4	4077
LPS059	115.3	135.2	1.5	996.9	1194.7	1022.8	1723.1	1265.3	2390.7
LPS060	163.3	268.5	0	1866.5	1707.3	1953.7	2184.7	2422.6	2990
LPS061	222.7	255.6	53.4	1448.5	2146.6	1600.7	1956.2	2511.7	3332.5
LPS062	136	228.5	99.1	627.1	863.2	467.7	1610.3	2304.9	2842.2
LPS063	299.7	251.8	226.3	796.8	1427	1771.5	1174.1	930	1433.9
LPS064	3079.8	4014.9	3039.3	7349.2	10807.8	7372.1	10515.8	4426.8	13038.7
LPS065	434.1	644.6	313.7	1147	1456.3	3097.5	2632.9	3695.2	1575.1
LPS066	214.7	171.7	134.2	0	69.3	249.7	726.1	871.9	586.6
LPS067	706.6	686.2	488.8	3013.5	2498.9	4522.1	4844.3	4782.1	5775
LPS069	199.6	172.1	123.9	75.4	19.4	269	874.1	854.6	0
LPS070	143.6	186.9	117.9	289.4	685.5	222.6	528.3	582.6	322.6
LPS071	180.4	170.2	187.2	157.2	183	882.3	326.7	508.4	310.2
LPS072	235.9	170.8	169.6	449.9	290.5	777.5	456.3	283.3	479.2
LPS073	900.4	1318.7	629.3	3416.1	4420.4	3894	4010.1	3367.3	4106.8
LPS074	27858.2	33812.3	32162.2	44513.2	111430.2	87262.8	47575.8	18233.4	66903.6
LPS075	2119.6	3296.9	1347.3	9540.3	5518.1	6367.8	10437.2	4054.1	9821.4
LPS076	347.6	336.3	218.5	2343.7	2326.5	1569	2415.2	1580.7	1990.4
LPS077	568.1	612.4	550.1	2908.9	1727.9	1660.2	2164.5	1798.6	2588.1
LPS078	3174.9	3137.6	3222.6	7616.1	6945.1	9024.5	11397.6	7995.6	26362.3
LPS079	1049	1066.4	302.2	4400.8	4126.8	4404.7	8203.7	4645.6	9377
LPS080	21208.7	28180.7	9065.4	39068.1	63741.1	37523.8	35948.5	11444.8	57266.6
LPS081	27381	33419.5	10292.3	43529.2	63629.5	28119	42128.9	15984.6	62043.4
LPS083	711.4	825	64.8	3306.9	3733.1	1898.2	3688.2	3407.5	3959.9
LPS084	216.4	211.2	21	1350.5	1724.2	1394.5	1965.6	2089.4	3604.5
LPS086	185.6	214.1	0	1808.2	1476	2915.6	2342.5	932.2	3339.1
LPS087	3404.7	5840.3	4144.1	12101.2	12860.9	14601.5	24953	5018.8	19643.5
LPS088	165.2	224.6	62.5	1497.7	2813.8	1593.8	3740.9	4017.3	3934.9
LPS089	223.8	213.7	0	1318.9	1574.5	2141.4	2443.5	3799.4	4185.6
LPS090	398.7	693.2	142.2	2593.7	2695.2	3465	3755.9	3638.7	3587.8
LPS091	391.2	700.6	270.7	1469.2	2092.2	3047.2	3754.2	3524.1	3149.7
LPS092	286.1	376.1	254.9	235.2	433.1	1353.8	1747.8	2658.1	3246.6
LPS093	185.6	273.7	126.3	114.7	296.8	254.7	412.1	1076.9	483.7
LPS094	232.8	261.8	151.7	274.3	249.9	641.1	891	577	1102.1
LPS095	199.3	191.7	91.4	25.7	169.9	433.7	813.4	1394.3	807.7
LPS096	97.9	139.2	63.2	0	162.4	159.2	504.6	752.3	150.6
LPZ001	150.8	207.8	257.7	202.6	485.5	704.2	555.2	1924.3	528.5
LPZ002	154.6	167.7	323.6	937.4	717.4	755.6	1068.8	1089.8	1107.7
LPZ003	1348.1	1781.1	609.3	5019	4261.6	6148.5	5600.4	3419.6	4858.4
LPZ004	2798.4	5533.1	2921.8	10703.8	8020.5	9958.4	10424.8	4135.9	14742.8
LPZ005	8403.4	19547.7	8589.6	32699.4	31426.9	21580.2	19437.9	8059.6	14660.3
LPZ006	360.6	2106.1	1173.8	7812.9	7966	11310.2	10516.8	4661.6	4618.2
LPZ007	272.5	409.9	454.7	2038.3	1107.6	2043.7	2073.5	2249.9	2751.3
LPZ008	207.7	258.2	212	1939.1	1482.6	1926.1	2243.5	1036	3324.9
LPZ009	745.1	496.5	633.9	4276.8	7474.5	9130.4	9814	5721.3	14116.8
LPZ010	893.7	1464.1	326.6	3759.5	4034	4261	4672.2	4388.6	9625.3
LPZ011	1829.5	2488.7	350.4	5922.7	4285.4	2984.2	5579.8	4236	9972.7
LPZ012	227.8	289.9	28.6	1885.9	1660.5	843.6	1913	1434.5	2785.5
LPZ013	247.7	213.8	84	1553	2015.3	1547.3	2567.6	3196.5	4347.7
LPZ015	261.7	315.8	55.6	2254.3	2409.8	2190.1	2562.4	1291.2	3237.3
LPZ016	2750.3	2151.8	3003.8	8316.2	6689.1	9147.4	9444.8	3349.6	8167.8
LPZ017	582.2	701.3	227.4	3830.1	3650.3	3828.2	4552.3	4574.5	4476.8
LPZ018	2867.6	6184.2	2746.8	10513.4	9443.1	10880.7	12748.3	5491.2	19422
LPZ019	7551.3	15875.3	9232.8	20440.4	22870.4	31026.1	33842	12823.6	38075.4
LPZ020	293.1	896.2	143.1	1661.8	2519.9	2987.1	4132.4	4022	3145.1
LPZ022	213.3	493.5	173.5	82.5	467.8	1355.1	1041.1	1481.9	1035.5
LPZ023	191.2	616.7	118.1	78.4	184	955.2	516.3	1254.6	574.4
LPZ024	142.6	321.7	118	0	81.9	826.8	195.8	763.9	491.7
LPZ025	661.9	764.4	536.9	1885.6	1791.8	3200.6	3017.8	4028.4	3897.8
LPZ026	194.7	221	150.4	1102	513.6	1714.4	1291.2	1625.6	980.7
LPZ028	301.3	424.2	210.9	1467.7	1654.3	2848.4	1937.1	4092.7	3086.2
LPZ029	132	151	124.8	319.5	644.1	478.7	452.4	564.8	709.3

TABLE II-continued

LPZ030	305.3	616.6	170.6	2800.7	2572	2485.4	1960.4	1425.4	2381.1
LPZ031	1945	3098.6	3636.7	12422.3	7673.2	8643.5	11552.7	4295.4	4600
LPZ032	26761.5	33518.4	33623.2	45482.1	106536.1	114284.5	46968.1	16371.6	42282.1
LPZ033	2068.3	1779.5	6651.8	7887.8	5249.8	9848.7	7632.1	4500.7	7710
LPZ034	221.4	363.3	216.3	2503	1949.2	1674	2078.9	1428.3	1774.9
LPZ035	110.7	156.8	85.2	836.6	512.1	1355.7	1217.4	294	1525.3
LPZ037	229.5	206.2	186.5	1422.1	1962.7	2742.9	3023	614.1	2895.5
LPZ038	605.7	722.8	352.5	3551.8	3072.2	3614.2	3266	2494.6	4039.7
LPZ039	366.4	964.6	177.1	3755.2	2744.9	4599.4	3589.7	2407.8	3925.2
LPZ040	185.6	278.3	100.8	2131.2	1321	1479.7	1654.6	773.7	2087
LPZ041	119.9	120.8	5	1199.8	1220.8	1090	1431.2	630	2206.1
LPZ042	61.9	121.9	2.6	731.4	1897.5	986.4	1366.1	458.4	2625
LPZ043	357.9	355.1	0	3236.5	2746.8	2960.1	3138.2	911.1	3345.6
LPZ045	738.6	1003.7	565.3	3866	3168.1	6406.2	4028.7	4526.2	4573.4
LPZ047	139.7	133.1	0	481.3	857.9	831.8	954.1	1926.3	3129.6
LPZ049	1396.5	2125.5	1496.9	4514.4	3629.8	5942.4	6898.6	3610.7	9214.2
LPZ051	264.6	610.7	205.1	826.3	1819.9	2243.8	3000.9	3400.7	2810.3
LPZ053	174.9	827.9	152	161.2	563.8	1149.7	1277.9	1243	1383.5
LPZ054	205.7	951	128.4	976.1	1901.4	1626.6	1265.8	1437.6	1328.8
LPZ055	135.2	389	168.5	420.2	524.3	1650.6	848.4	1200.6	914.2
LPZ056	190.2	323.3	229.5	439.9	664.2	1613.1	1014.2	1727.3	1126.2
LPZ057	87	199.9	180.1	2154	863.7	3059.1	2994.9	2696.3	2990
LPZ058	139.3	227.5	55.3	1695.1	902.5	2426.6	2195.6	1925.4	1598.2
LPZ059	173.4	289.6	189.4	891.7	759.7	1835.3	1332.9	962.5	1286.6
LPZ060	301	464.8	114.1	2296.5	2860.4	2786.6	2974.4	1629.6	2301.9
LPZ061	1212.2	1711.1	794.4	7468.5	5190.1	7957.5	5857.5	2819.8	3922.3
LPZ062	2078.9	3648.3	2499.3	14932.7	7691.9	9294.1	9213.3	3077.8	4850.3
LPZ063	641.6	984	2114.2	5547.2	3688.6	6191.3	4844.5	4058.7	4162.4
LPZ065	520.2	443.3	332.3	2720.4	1816	2848.5	3320.4	4501	3948.4
LPZ066	663.7	357	356.6	3458.6	2196.3	3567.6	3081.4	1325	2388
LPZ067	1469.5	2582.6	3152.4	8674.9	8080.1	9367.6	8556.2	4135	7240
LPZ069	211.4	283.6	0	1921.6	913.1	1567.5	1866.5	1043.3	2269.1
LPZ070	229.6	334.9	2.8	1659.3	1254.6	1681.6	1883.6	1360.7	2442
LPZ071	332.3	633	15.7	3126	2729.9	3290.2	2998	2011.7	2744.8
LPZ072	39	38.9	0	581.2	1401.7	1307.1	1089.7	710.4	1866.3
LPZ073	131.3	250.9	4.4	1176.4	2903.2	2356.7	1718.3	985.9	2700
LPZ074	92	116.5	0	355.6	1643	1041.3	1027.4	1042	2553.6
LPZ075	195.9	0	0	0	474.7	488.1	847.6	1488.4	2755
LPZ076	232.4	134.5	730.7	0	268.9	0	568.3	1007.4	2624.4
LPZ077	1143.1	2350.7	187.5	6551.1	5960.9	5520.2	7189.6	3483.6	7931.5
LPZ078	851.5	1021	873.3	3011.7	4619.7	5273.6	6408.3	3950.1	8831
LPZ079	281.6	779.7	315.9	1296.6	2065	2090.8	2287	2271.9	1824.5
LPZ080	1653.5	3124.5	3778.7	8321.1	7987.7	10470.3	8085.7	4454.9	8067.4
LPZ081	92.6	292.7	161.8	746.8	903	1558.5	1410.8	746.1	1230
LPZ082	123.2	430.5	240.1	1907.9	1283.9	2707.5	1801.7	948.9	1634
LPZ083	77.8	183.2	120.2	4010	2437.2	4390.6	3649.7	3983.1	7032.5
LPZ084	1272.3	956.1	1297.2	5881	4505.3	10642.2	9798.6	3938.5	8446.3
LPZ085	321	466.2	457.6	4324.8	4008.4	6890.5	4599.7	5672	10082.2
LPZ086	1529.6	3587.2	3236.8	10729.4	10010.2	10739.2	10634.9	4674.2	11980.7
LPZ089	614.3	500.4	601.9	4196.2	3890.5	4405.8	4331.9	3066.9	3960.3
LPZ090	643.8	1177.5	1315	4017.8	4456.2	6394.5	4824.4	3000.1	3538.3
LPZ091	1006.7	1754.2	4090	11615.8	11728.5	16837.8	14461.9	5005.1	14726.4
LPZ092	419	528.6	1336.8	4158.4	3568.1	8393.4	8192	4638.4	3939.4
LPZ093	162.2	453	90.9	1436.5	899.2	2218.6	1798	741.8	1789.8
LPZ094	123.1	197.1	0	1355.7	779.4	1360.5	1713.8	794.4	1597.8
LPZ095	94	130.6	3.5	1099.9	737.4	558.3	1473.4	871.4	1809.3
LPZ096	314.3	327.5	22.1	2574.2	1620.9	2748.1	2533.9	1858.4	2979.9
LPZ099	231.7	359.8	6.2	1456.9	1335.7	1672.4	2170.8	2160.8	2755.8
LPZ100	375.6	650.4	136.7	2834	2518.6	3053.2	3159.8	2841.2	3453.7
LPZ101	217.1	425.7	11.8	2769.3	3312.6	2556.3	5262.5	1501.2	2947.3
LPZ102	294.3	289.2	55	1803.6	2764.5	2532.5	2613.4	2447.6	3377.6
LPZ103	224.2	92.8	17	989	1850.6	1643.7	2303.4	3729.5	4029.5
LPZ106	328.4	158	57.5	912.5	1239.6	1214.5	1669.6	2062.3	4720
LPZ107	25137.4	28865.6	19438.9	43316.7	75674.1	58296.4	45927	3332.1	64391.6
LPZ108	1132.8	2084.1	330.6	4299.2	3629.8	4480	6406.5	3235.2	9993.6
LPZ109	548.8	1356.1	417.7	3237.9	2581.9	3177.5	3977.1	1874.2	4107.7
LPZ110	379.7	1132.3	220	3941.9	2720.7	4103.6	3563	2245.7	3031
LPZ111	157.5	383.2	200.3	1188.3	749.8	1675.7	1926.1	1685.1	1655.3
LPZ112	332.1	522.9	220.7	2950.9	2223.9	2257.5	2856.4	2632.8	2711.8
LPZ114	590	151.8	217	4659.6	3824.5	6848.2	7228.9	2831.3	9446.9
LPZ115	6268.6	3368.3	8724.6	25695	19481.5	33011.8	32267.9	2903.4	52760.4
LPZ116	891.2	766.7	1481	6455.1	3684.7	5597.5	8456.7	1682.9	10139.2
LPZ117	529.8	826.6	126.5	3706.8	2663	2897.5	3996.1	1807.3	2635.2
LPZ118	437.8	628.1	122.1	3903.5	3245.2	3529.9	3500.1	3506.1	2867.9
LPZ119	331.3	755.1	83.1	3781.2	4072.6	4024.9	3449.9	3742.2	2533.9
LPZ120	196.5	796	181.4	4219.4	3297.7	4322	4539.3	2622.7	3763.6
LPZ122	154.4	208.4	158	2332.3	1468	3044	2838.8	2112.5	2323.6
LPZ124	172.9	420.1	136.6	2319.5	1539.3	1722.7	2453.6	3109.1	2297
LPZ126	446.5	604.2	187.3	3859.4	3120.8	2816.9	3324	2181.4	3237.7

TABLE II-continued

LPZ127	439.3	499.4	53.5	3781.8	3083.3	3769.8	3848.4	1729.6	2902.2
LPZ128	1022.3	1063.8	447.9	3904.9	3753.5	5579.6	4534.2	2133.1	5843.6
LPZ131	249.6	373.8	27.3	2170.1	1551.6	1611.4	3077.3	2946	2409.5
LPZ133	325.3	328.7	42	2706.9	2358.1	2131.3	3257.2	2598.7	2144.3
LPZ136	263.6	384.1	0.9	2377.3	3386.4	2044.7	2726.4	2398.2	2570.6
LPZ137	351.6	402.6	91.9	3435.9	3122.8	2406.9	3054.7	3392.1	3216.6
LPZ138	1047.7	936	530.3	3920	3091.2	2507.9	4249.5	3109.9	4758.4
LPZ140	379.9	456.6	105.6	1936.7	3674	2908.4	3678.1	3663.2	4481.7
LPZ141	715.4	1341.8	536.4	4712.8	3615.6	3746	4815.5	4533	8229.3
LPZ143	3251.1	4810.8	2848.5	9675.1	8289.6	9486.6	12270.6	4424.9	28251.9
LPZ144	386.2	1338.3	294.1	3433.8	3015.7	3333.7	4618.9	3699.7	6825.1
LPZ145	277.5	1064	536.5	3072.3	1155.6	2977.7	3188.2	7388.2	3013.6
LPZ146	128.5	362.8	139.5	2224.4	1364	2125.6	2428.3	3465.8	2351.1
LPZ147	266.5	544.2	241.3	3318.1	2241.9	2162.6	2908.8	3252.6	2525.6
LPZ148	725.8	725.5	290.2	5002.2	3682.1	6542.3	6927.9	2903.1	10410.9
LPZ149	2492.7	3102.7	1052.7	8980.9	7669.2	7185.3	9921	7375.4	12848.8
LPZ150	5257.3	7586.3	3221.3	15156.2	12776.8	7401.2	14686.5	1570	20635.9
LPZ151	1384	2049.2	1128.3	5576.7	3853.7	3780.3	7227.3	3206.7	7702.7
LPZ152	975.8	1300.2	546.4	5096.1	4344.9	4302.5	4960.3	1566.2	4223.4
LPZ153	13378.6	22235.1	10073.1	33495.1	50802.7	28291.5	29602.5	3224.1	40232.7
LPZ154	663.3	738	430.3	3847.3	3880.2	6253.9	4707.7	5341.9	3393.8
LPZ155	1121.7	612.7	748	3902.3	4289	4676	5328	6964.2	5353.5
LPZ157	1157	957.9	762.2	4218.8	4266.6	3777.2	4583.7	5017.5	4396.6
LPZ158	13278.5	17582.9	9898.7	32456.5	42805.1	24534.6	31442.6	4152.5	36015.3
LPZ162	3407.5	5943.1	5126.6	10324	11710.9	7727.6	7572.2	2312.6	9394.1
LPZ165	1419.4	1550	693	4519.9	3692.9	6102.1	5617.1	3061.3	4706.4
LPZ166	2642.1	3504.9	1288.6	7134.8	6994.5	5170.5	10453.3	4932.9	15993.7
LPZ167	980.4	1518.1	564.7	4902.6	4803.7	3343.6	4869.5	4421.2	6582.2
LPZ169	621.8	792.7	93.4	3562	4266.3	1794.9	3496.3	4238	3143.7
LPZ170	1009.3	1405.3	695.2	5793.7	4469.2	4952.7	6239.7	3914.1	6782.3
LPZ171	1064.6	968.6	1050.7	4110.8	3903.7	5467.2	5659	3164.1	6795.3
LPZ172	1233.3	1113.3	401.8	4207.9	7922	8417.5	10419.2	7983.5	15065.2
LPZ173	3333.8	5236.8	6072	9552	8880	8653.2	13461.6	2408.7	25719.1
LPZ174	486.7	1263.6	143.3	3318.2	2027	3632.3	4245.3	6086.4	8781.2
LPZ175	594.7	1487	520.8	3051.5	3610.8	1846.4	3642.9	4048.5	4329.5
LPZ177	167.3	481.7	234.5	1955.9	1139.2	907.8	1452.9	4462.5	1762
LPZ179	1231.4	1583.2	835.8	5029.7	3654	3871.7	3248.8	2741.9	2853.2
LPZ181	2259.5	4282.9	774.8	8911.6	8788.6	6833.3	5825.5	3398	3922.8
LPZ182	1194.7	2289.6	673.8	8220.3	5601.2	5869.3	5572	1808.4	7607.9
LPZ186	6255.6	6866.5	6841.1	24861.8	16742.4	23502.2	17304.6	1750.4	27328.9
LPZ189	27581.8	34787.4	31889	45673.7	106688	95043.9	46998.5	3548.1	67943.9
LPZ194	673.9	904.9	528.7	4064.5	3530.2	3160.6	5095.2	4531.1	3492.1
LPZ195	898.9	889.6	675.7	5606.3	4004.3	5230.5	5721.4	4908.1	4940.9
LPZ196	1073.7	1935.1	558.2	3941.1	3672.6	3681.6	5977.8	3059.7	5050.3
LPZ197	488.4	522.5	386.6	2613.4	1684.4	3541.4	3507.4	4980.8	2763.1
LPZ198	575.6	733.1	299.6	4152.3	2411	2916.8	3872.4	6530.7	2931.8
LPZ199	390.7	442.5	222.4	2704	2176.2	3159.7	2957.1	5357.6	2983.4
LPZ201	2255.7	3876.6	347.6	10222.9	6897.7	6294.3	7324.7	3549	3857
LPZ202	25939.2	34864.8	28937	43395.9	85136	71116.8	38688.5	2676.2	14449.1
LPZ203	4917.3	4458.1	2603.2	10348.3	6571.1	8325.7	11034	5453.1	6598
LPZ204	27637.2	31853.9	22475.7	43983.9	89520.6	46504.2	44333.5	7963.6	58054.1
LPZ205	1184	1084.2	327.7	3901.8	4402	3125	4598.2	4501.5	4714.2
LPZ206	1309.8	1509.5	367.3	3961.5	3983.3	3079.6	4196.2	3641.4	3247.6
LPZ207	27569.1	30446.2	27094.6	45211.6	90196.1	58153.8	46488.1	9879.3	64709.2
LPZ208	22722	28208.9	30019.5	40314	74354.1	37339	33919.6	3989.8	56683.6
LPZ210	1015.1	1789.8	196.8	5006.3	6159.7	3067.8	4944	4347.5	6846.4
LPZ211	277	327.3	519.4	2540.7	1788.5	3048.6	1110.8	2577.4	3506.6
LPZ212	1095.5	865.5	930.6	4051.6	4491.6	2857.6	6348.1	4078.7	16174.9
LPZ213	376.6	539.3	339.6	2503.1	1540.8	1333.7	3082.2	6024.3	4163.1
LPZ214	137.5	306.1	190.1	1915.6	866.1	1280.9	1240.8	6372.4	2111.8
LPZ215	3519.4	3120.9	3300.9	16939.5	15489.1	10948.6	12502	3515.1	16236.4
LPZ216	26761.3	34226.4	28477.9	42274.8	67630.3	41420.3	36331.4	1433.8	17109.4
LPZ217	15563.1	21739.4	12259	26824.9	34266.3	9429.4	28156.7	1339.2	41568.4
LPZ219	2404.9	3704.5	2084	8575.1	8573.2	6237	11757	3255.4	13484.9
LPZ220	3617.2	6998.6	7957.2	13960	9400.8	3432.3	10805.5	3551.7	12867.4
LPZ221	482.6	478	1405.6	3296.5	3079.8	3312.5	4143	4429.4	3267.3
LPZ222	318.3	524.5	406.6	3011.7	2309	3811.8	4199.4	5319.9	3292.3
LPZ223	367.7	633.2	437.7	2752	1970.3	3767.4	2514.2	3672.3	2163.1
LPZ224	337.9	1030.2	317.2	2701.2	1798.7	7393.6	2962.5	7876	3353.7
LPZ225	3288.1	3590.3	2912	8781.8	7400.7	2317.1	11370.2	3186.6	22244.6
LPZ226	325.6	361.4	128	2467	1263.7	10190.1	1636.3	3808.8	1166.9
LPZ227	2175.5	6375.8	458.8	6316.2	6632.1	9013.9	6614.3	3901.2	2588.2
LPZ228	2638	3701.7	500.1	5991	4819.8	5747.8	7102.5	3182.5	4185.4
LPZ231	1631.7	2090.4	260.7	5811.5	4749	2530.8	5033.1	3191.3	3810.5
LPZ233	1596.6	1223	296.6	4355.6	3818.9	2988.8	3749	3324.7	3855.2
LPZ234	1734.3	1479.2	219.6	5058.5	4614.4	2034.9	4992.1	1979.9	5152
LPZ235	626	635.9	185.9	4066.8	3255.5	4035.7	3368.7	2880.8	3643.5
LPZ237	1677.8	1385.3	847.4	4536	3702.8	2943.6	4886.5	2307.8	5136.8
LPZ239	673.4	407.8	245.8	2981.9	3199.2	2781.6	4235.6	2342.6	4863.7

TABLE II-continued

LPZ240	387	247.4	254.8	2075.8	2317.4	2894	2721.7	2054.5	4317.9
LPZ241	258.3	337.8	110.9	3503.1	3829.6	22593.5	1889.5	1315.9	8842.6
LPZ242	4315.9	2560.2	22.5	12510.2	12605.3	2345.2	16197.1	1114.8	39684.4
LPZ243	174.8	274.4	23.1	2193.6	346.2	2395.7	1366.5	2568.2	3103.8
LPZ244	417.5	269.1	3458.5	3545.1	1831	2834.7	1781.1	7589.2	5662.7
LPZ246	889.5	918.7	2302.7	3920.3	3228.9	4409.3	3536	1258.8	2645.3
LPZ247	1203	2088.9	46.7	4956.9	4253.2	3559.7	4570.8	1702.6	3350.6
LPZ248	973.3	1338.1	86.2	3977.4	4392.8	2033	4094.9	2062.6	4279.9
LPZ249	361.3	324.3	206.7	1948.6	1764.3	2098.7	2762.1	1643	2862.4
LPZ250	267.6	487.8	118.7	2690.4	1522	2989	3121	1928.9	1809.7
LPZ251	245	279.7	168.5	1409.9	555	9932.3	2552.5	3050.3	1371.1
LPZ255	2021.3	2488.5	334.1	7289.5	7773.7	1269.1	9020.3	4492.4	10134.6
LPZ256	67.1	72.2	296.7	412.2	229.8	922.7	570.3	5040.6	1263.9
LPZ257	167.3	146.9	482.6	521.8	102.5	2699.4	599.8	2362.1	1553.4
LPZ258	247.5	236.5	69.7	1429.8	974.6	971.9	2668.7	2990.8	3445.9
LPZ260	98.1	188.8	463.1	377.1	337.2	880	808.9	1552	1084.6
LPZ261	73.7	20.5	386.3	1143.6	50.3	4443.8	903.3	2309	1341.6
LPZ264	482.7	528.5	1151.3	3659.7	1972.6	9892.4	2831.4	1584.4	3208
LPZ265	534.6	647	457.6	4473	4089.9	656	5899.6	2972.2	5649.8
LPZ266	16.9	61.2	1062.3	876.1	1183.4	1624.3	663.3	622.4	1609.7
LPZ268	143.7	142.9	255	1983.5	810.3	9809.8	1293.5	1757.3	2177
LPZ269	1747.5	1271.8	1636.4	7364.1	5108.7	6903.3	11401.2	3774.1	14643.8
LPZ270	373.8	77.9	1901.2	5015	3872.6	3485.9	5621.1	4284.8	5197.8
LPZ271	705	473.1	315.6	2863.8	2625.4	2120.5	4048.2	1424.9	4291.1
LPZ272	2809.4	2423.8	300	5056.2	2463	3534.6	3496.9	609.7	3996.8
LPZ273	219.8	162.4	242.4	90.2	130.2	3251.3	166	1193.5	1836.5
LPZ274	489.2	367.7	284.6	991	1104.2	395.9	2282.3	747.2	4535.7
LPZ275	93.5	140	156.8	433.3	217.1	0	837.9	1056.2	2352.3
LPZ276	53	109.7	106.8	0	0	0	369.1	1303.6	1897.6
LPZ277	105.9	159.4	68.7	0	0	230.1	236.2	706.1	1337.9
LPZ278	65.7	48.3	156.4	0	0	1788.2	406.3	1442.3	1564.1
LPZ279	214.7	212.2	75.3	1356.3	790.8	5213.3	1722.4	496	2426.2
LPZ280	156.2	247.7	1553.6	3510.5	2515.1	289.7	3182.1	612.7	3123.7
LPZ281	34.6	92.1	73	0	0	1648.3	565.5	522.8	543.3
LPZ282	200.9	187.7	218.1	536.6	205.9	7324.8	1145.4	2977.5	957.5
LPZ283	1833.5	1880	775.8	3303.2	5113.2	527.6	5281.2	324.5	3806.8
LPZ284	215	0.6	148.8	0	29.6	848	408.4	148.8	1294.3
LPZ286	219.7	21.9	13.6	234.9	78.6	2703.6	198.4	947.9	1233.2
LPZ287	112.6	126.2	36.5	1170.3	459.9	306.3	157.5	1173.7	1821.3
LPZ288	23.6	62.2	37.5	774.1	639.3	792.6	715.8	1422.6	1169
LPZ289	44.1	13.1	107.4	323.4	95	9975.4	889.5	2240.6	1894.9
LPZ290	1324.7	1572.4	1838	6941.6	4616.9	2995.3	11538.8	407.1	12699.5
LPZ293	45.2	246.3	145.6	2785.5	1923.1	0	3185.6	0	3550.4
LPZ294	0	19.8	0	403.3	280.4	89.1	785.9	551.6	1378.4
LPZ295	40	24.5	0	169.9	26	1324.9	1058	848.8	1406.5
LPZ297	385.6	127.6	17.4	1238.5	941.5	0	2680.9	2084.3	4065.3
LPZ299	106.9	36.2	0	0	926.2	0	1060.7	1854.9	1575.9
LPZ300	73.2	93.2	80.2	0	1143.6	1053.3	1034.5	2304.9	2120.8
LPZ301	126.2	0	5.8	161.2	1245.7	516.3	1612	761.3	2826.1
LPZ303	83.1	488.8	98.6	0	73.5	979.9	538.7	510.7	1214.7
LPZ304	213.7	498.3	137.6	1028.6	0	5405.8	860	2212.1	2201
LPZ306	1439.4	1735.3	2526.4	4212.7	3140.4	2090.1	8128.5	4874.6	14413.9
LPZ307	534.1	710.5	515.5	2785.3	734	0	2137.3	1692.8	3540.3
LPZ308	116	304.4	137.7	151.8	28.2	364.2	621.1	631.4	851.2
LPZ309	80.1	137.2	92.7	0	0	2648.1	529.4	192.6	735
LPZ310	430.8	584.9	799.2	1887.2	1887.1	6161.2	2974.3	3575	2426.6
LPZ311	690.5	995.7	208.4	3725.8	2843.8	0	4329.3	3620.8	4170.1
LPZ312	109.8	334.2	34	72.5	4.5	1489.3	140.1	431.6	744.8
LPZ314	26.5	200.1	3.3	181.2	0	1231.5	331.5	440.1	804.6
LPZ315	305.8	211.3	147.5	811.2	1008.1	3797	2231.8	1438.8	1881.8
LPZ318	621.3	715	337	3488.2	2480.9	781.9	4326.1	4824.7	6969.2
LPZ320	214.8	92.2	9.9	1170.9	54.5	4501.5	1122.3	1169.4	1696.6
LPZ321	880.4	755.2	1899.3	6166.2	5105.8	411.6	6096.5	4853.6	6057.2

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TABLE III

LSC Media	Multiplication Media		Maturation Media
Components (mg/L)	16	1133	923
NH_4NO_3	603.8	603.8	200.0
KNO_3	909.9	909.9	454.95
KH_2PO_4	136.1	136.1	136.1
$Ca(NO_3)_2.4H_2O$	236.2	236.2	59.05
$MgSO_4.7H_2O$	246.5	246.5	246.5

TABLE III-continued

LSC Media	Multiplication Media		Maturation Media
Components (mg/L)	16	1133	923
$Mg(NO_3)_2.6H_2O$	256.5	256.5	256.5
$MgCl_2.6H_2O$	101.7	101.7	101.7
KI	4.15	4.15	4.15
H_3BO_3	15.5	15.5	7.75
$MnSO_4.H_2O$	10.5	10.5	10.5

TABLE III-continued

LSC Media	Multiplication Media		Maturation Media
Components (mg/L)	16	1133	923
$ZnSO_4.7H_2O$	14.4	14.4	14.4
$NaMoO_4.2H_2O$	0.125	0.125	0.125
$CuSO_4.5H_2O$	0.125	0.125	0.125
$CoCl_2.6H_2O$	0.125	0.125	0.125
$FeSo_4.7H_2O$	6.95	6.95	41.7
Na_2EDTA	9.33	9.33	55.9
Sucrose	30,000	30,000	—
Maltose	—	—	20,000
myo-Inositol	1,000	1,000	100
Casamino acids	500	500	500
L-Glutamine	450	450	450
Thiamine.HCl	1.0	1.0	1.0

TABLE III-continued

LSC Media	Multiplication Media		Maturation Media
Components (mg/L)	16	1133	923
Pyridoxine.HCl	0.5	0.5	0.5
Nicotinic acid	0.5	0.5	0.5
Glycine	2.0	2.0	2.0
2,4-D	1.1	1.1	—
BAP	0.45	0.45	—
Kinetin	0.43	0.43	—
Polyethylene glycol	—	—	130,000
ABA	—	5.2	5.2
Gelrite	2,500*	2,500*	2,500
pH	5.7	5.7	5.7

*For solid media only

TABLE IV

Description of clones used in hybridization study shown in FIG. 9.

Clone #	Homology	Description	ID with Arabidopsis	Score	E-value
PC04B12 ('LEC' in figure)	Lotan et al. 1998. Arabidopsis LEAFY COTYLEDON 1 is sufficient to Induce Embryo Development in Vegetative Cells. Cell 93: 1195–1205	Required for embryo maturation & Cotyledon identity. Ectopic expression induces embryonic differentiation traits in transgenic seedlings.	79% ID, 93% + ve over 96aa	171	7e–44
ST17B05 ('PLK' in figure)	PICLKE/CDH3, Chromatin remodelling. Ogas et al. 1999. PICKLE is a CHD3 chromatin-remodeling factor that regulates the transition from embryonic to vegetative development in Arabidopsis. PNAS. 96(24): 13839–13844	The pickle mutants express embryonic traits after germination, Represses lec expression	50% ID, 74% + ve over 155aa	166	1e–41
PC08C06 ('FIE' in figure.)	FIE, fertilization-independent endosperm protein. Ohad, et al 1999. Mutations in FIE, a WD polycomb group gene, allow endosperm development without fertilization. Plant Cell 11(3), 407–416	Fie mutants initiate endosperm development w/o fertilization	61% ID 75% + ve over 67aa	92	8e–20

Table 4. Description of clones used in hybridization study shown in FIG. 9.

TABLE V

Cell Line (Stage of Development)	488 (Liquid Suspension Culture: Stage 1–3)	499 (Liquid Suspension Culture: Stage 1–3)	499 (Liquid Suspension Culture: Stage 1–3)	500 (Liquid Suspension Culture: Stage 1–3)	500 (Liquid Suspension Culture: Stage 1–3)	260 (Stage 7)	260 (Stage 9)
Media	1133	16	1133	16	1133	Maturation	maturation
# Embyros	(49.5)	118.5	(129.5)	187.75	(147)	Na	na
'FIE'	++++	+	+++	+++	+++	+++	+++
'LEC'	(++)	++	(+++)	++	(+++)	+	+
'PKL'	++++	+	+++	+++	+++	+++	+++

Table 5. Table of data from FIGS. 9a & b. Numbers (488, 499, 500, 260) refer to different cell lines. Liquid Suspension Culture contains early-stage embryos (stage 1–3) Embryo number refers to the number of late-stage (stage 8–9) embryos produced by each cell line when matured according to Pullman and Webb (1994). + = low expression, ++ = medium level of mRNA, +++ = high level of mRNA, ++++ = very high level of mRNA. Circles around certain + signs, see text. Na = not applicable. Levels of mRNA are relative and refer to the experiment depicted in FIGS. 9a & b.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 339

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<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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aagatcacat accaggtgtt ggagcagatt cgatagatat tgaagatatg aagccaagga 180

gtggagcagt tattgaaaag ggcacaaaaa aatttgccat ttacaaagat gaaaatgggc 240

tgattcacaa atactcggca atatgcccac acatgaactg tattgtgaaa tggaatccta 300

tagactcaac tttcgattgc ccctgccatg gttcaatgtt tgataatctg ggtcgatgca 360

tcaatggacc tgccaaggcg gacctatttc ccgaagatta acgatagttg tttgtacatg 420

taattatctt gatattgtat atatatgtat ttaaattata cagtacaata aatccatgtt 480

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aaaaacgcca tagcgacgga tgactgtaaa tccttaggga cggatgactg taaatcctta 180

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<400> SEQUENCE: 3

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atggggattc accagttttt gtagaatttg caatcatcgg atgacaattt caaagttttc 180

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atcttttcag ttggcaaaaa aaaaaaa 267

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gacgtgtaaa cgacgccagt gatgtatacg aatcactata ggcgatggcc ttctagatgc 120

-continued

atgctcgagc gccgcagtgt gatgaattgc agaatcggct ggtactcacg ggctagagaa 180

aggcacaagc actttttgtc attttaggat cagaggcatt caggtatagg aagggtggct 240

cagataggca gatggatcgg cattttgccc agtcatgaaa cattttatgc atgttattgc 300

ctcccaagga cgaaatcagt tctttgtgcc ttctggtgat atcacttcaa acaaaaggca 360

acagttctgt gatttcatat ggtttgtcac tgaatatttt gttgcagatg ttctctacta 420

ttttttatct gctttcaagt gattatttgt tgattcccca tggatagtta tgctaatcag 480

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ccaaagagtg gaatgcttta ttgaccagca agaccttgaa atttttataa ccaatgccca 180

tcaacagagc ctttcttaaa aaacgcaaag cccagctctg tcaccttatt agttagtata 240

aactgacatt cttccaagct tgtgtgcgca gaaacaataa agaacttcac cttggtttaa 300

agaacgtgcc atgaagaaaa cgtcccaaga aaaatgaaat ggctccttcg accattcagt 360

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<210> SEQ ID NO 6
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 6

ggtactccac gggctagaga aaaggcacaa gcacttcttc gtcattttag ggatcagagg 60

cattcaggta taggaagggg tggctcagat aggcagatgg atcggcattt tgcccagtca 120

tgaaacattt tatgcatgtt attgcctccc aaggacgaaa tcagttcttt gtgccttctg 180

gtgatatcac ttcaaacaaa aggcaacagt tctgtgattt catatggttt gtcactgaat 240

attttgttgc agatgttctc tactatttttt tatctgcttt caagtgatta tttgttgatt 300

ccccatggat agttatgcta atcagttgca tttctcttgt accagtcaac aaacaaaaat 360

gcttgtagga atccattact atttattttc agacaggtaa acgtgtagct aattgttctg 420

gcaaaaaaaa aaaa 434

<210> SEQ ID NO 7
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 7

acgacgtgta aacgacggcc agtgattgta tacgactcac tatagggcga ttggccttct 60

agatgcatgc tcgagcggcc gcaggtgatg gatatctgca gaattcgctt ggtactccac 120

ggctagagaa aaggcacaag cacttcttcg tcattttagg atcagaggca ttcaggtata 180

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ggaagggtgg tcagataggc agatggatcg gcattttgcc cagtcatgaa acattttatg 240

catgttattg cctcccaagg acgaaatcag ttctttgtgc cttctggtga tatcacttca 300

aacaaaaggc aacagttctg tgatttcata tggtttgtca ctgaatattt tgttgcagat 360

gttctctact atttttatc tgctttcaag tgattatttg ttgattcccc atggatagtt 420

atgctaatca gttgcatttc tcttgtacca gtcaacaaac aaaaatgctt gtaggaatcc 480

attactattt attttcagac aggtaaacgt gtagctaatt gttctggcaa aaaaaaaaaa 540

<210> SEQ ID NO 8
<211> LENGTH: 794
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 8

ggtactccac gaagcaaaaa gagtcagggg aatgaagatg gggggctccg acaagaagcg 60

gatcagagaa gagcaggaaa tgagtccacc tgaggaatcc tggagacaga aacaggggcg 120

tttaatggag tttgaggcag ggatggccta tgataaacct gaaaatgccg gtgcaggtaa 180

tgagaatttg ccagagtttt gctctctttc aaatgagtac tcgatgttat tgaaagatcc 240

atggagttgg gaggatagca ctggtttcgg aatccgaagc ttagctgctg tcaggaagca 300

gtcttgtata ttggactatc tccatgattc tgctgtagat aatcgctgtg aaaaggattt 360

tgccgagcag cacaaggtac aggaagagga ggattgtttg agaaggtctc tttttgaagc 420

cacagatgat cagctctgga ggcttcagag tctttgcagg atacagaagg tctgtttcct 480

ctggattccg tgggtagcca tgattgcacg accttgttgc aggatgagag cattgttcag 540

ggcgctgctt cttacttcag aatttgggaa caggatgatg gtcacaagga tgccaaaatt 600

catgaagatg gcattggttt tgtgtatggg agtgggatct cggattggat tcggagggct 660

ccctcgaatc aatctgagtt ttctgaatct gttgaatttg aaagctctat gttttcactg 720

taatttgggt ctttttaatt tcttcctatg taatttgggt gtttctaatt tcttccttca 780

gcaaaaaaaa aaaa 794

<210> SEQ ID NO 9
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 9

ggtactccac catatccagg taaacaaggg aaaacagagt cagcttctag tatgttgtat 60

gccttgctct gtctgttttc tttgatcttt gatgccaagc aagttgaatg tgatcactaa 120

atgttgctgg cagtagagct ggagatgtgc tgtctctttg gtgtcattag cacagaagct 180

attggagaaa tgattattat ctgtttgata acttctagag cattttttctg cttccaattc 240

cacaaggtgg aaagtgcaag gatgtttact ttcttaaact gtacttgcct tgtatttgat 300

gatgtaaggt tgtgtggcaa aaaaaaaaaa 330

<210> SEQ ID NO 10
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 10

ggtactcacc atatccggta acaagggaac aagtcagttt tagaaagtgg acccccggtt 60

ccgtcgtttt cttgatctcg gagccaagca agtggatgtg atcactaaat gttgctggca 120

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gtagagctgg agatgtgctg tctctttggg tcattagcac agaagctatt ggagaaatga 180

ttatggtatt ccaccatatc caggtaaaca agggaaaaca gagctcagct tctagtatgt 240

tgtatgccct gctctgtctg ttttctttga tctttgatgc caagcaagtt gaatgtgatc 300

actaaatgtt gctggcagta gagctggaga tgtgctgtct ctttggtgtc attagcacag 360

aagctattgg agaaatgatt attatctgtt tgataacttc tagagcattt ttctgcttcc 420

aattccacaa ggtggaaagt gcaaggatgt ttactttctt aaactgtact tgccttgtat 480

ttgatgatgt aaggttgtgt ggcaaaaaaa aaaaa 515

<210> SEQ ID NO 11
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 11

ggtactccac catatccatg taaacaaggg aaaacagagc tcagcttcta gtatgtagta 60

tgccctgctc tgtctgtttt ctttgatctt tgatgccaag caagttgaat gtgatcacta 120

aatgttgctg gcagtagagc tggagatgtg ctgtctcttt ggtgtcatta gcacagaagc 180

tattggagaa atgattatta tctgttacat aacttataga gcatttttct gcttccaatt 240

ccacaaggtg gaaagtgcaa ggatgtttac tttcttaaac tgtacttgcc ttgtatttga 300

tgatgtaagg ttgtgtggca aaaaaaaaaa a 331

<210> SEQ ID NO 12
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 12

ggtactccac tagaccgggt agggtctctc catggttttg cgacttaggt taggtgtcct 60

gttctgttaa tgattttgag gttttgtaat tgtgagtatg tttccagggt tttgaacctg 120

ggtactcggc ctttgttgga atgtagtctg gttaatttat atgtatatgt aaccttgggg 180

tttcgagccc agttctctgt tcttcttgaa atgaaatgcg atttgttcta aaaaaaaaaa 240

a 241

<210> SEQ ID NO 13
<211> LENGTH: 247
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 13

atatatacgt atggtattcc acagcatgaa ctcttcgaca ttatatgctt gttatagttt 60

ttaagagagg agacttacct cacacatgta cagcttttta ttgtcgtgct ttcagttgat 120

ggatgattgt tgtagtcctg tcattggttg gacaattttc atcatcctaa agatccaaga 180

attcatgtgg caagaaactt taataaagtc aaatataatc cgatgacgta accctaaaaa 240

aaaaaaa 247

<210> SEQ ID NO 14
<211> LENGTH: 197
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 14

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ggtactccac tagtgatcga ttctctgtat gtgacgctgc gcggcggctt atagcgcttc 60

actgagaatg tacggtatat tatgattgat gtgatggatt tgctccgcag cttcggctgt 120

tgtatctgct cacttcggcg tatatatgta atatgttgct tcttcagaga gatgaacttc 180

cccctaaaaa aaaaaaa 197

<210> SEQ ID NO 15
<211> LENGTH: 177
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 15

atagatcatt ttaaagtttc agtgatttga atctaattcc actgcatttc ctcgcaaact 60

ggcagtcaaa tagtattccc tctttcagtg acaggctggc aggtgtttca ttcttataca 120

aacatgatta tcataattcc attaattcat ggcgttttct ttgccaaaaa aaaaaaa 177

<210> SEQ ID NO 16
<211> LENGTH: 475
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 16

ttttttttttt ttagggagaa aggtaacttc agccagcttt caaaggcaac acctacaaaa 60

ggggtgactg agaactcaga cacagacgac aagtgatcat tcgggccaga tttttgttga 120

gagagttgta gtgtgtaatt gattcatttc atacatttga tatgcaagcc tgtacaatag 180

cctgtgactg ttaagggcat tcttttgtct ccctgttgct atttgggttt ccggtgtgtt 240

cattttcact tatttttgtg ttttagctgg aagaatttga gagggtagaa ttgtgtcatc 300

gctatggctt gtgcatgact catgagccag cagttgaaac ttttatttat taagttataa 360

tactatgtct tgtcaattct caataaaaga tattttatgc tgttgggcag catctaaaat 420

gttttgtatg ttagcataaa atcccatttt ctataagttt ttgccaaaaa aaaaa 475

<210> SEQ ID NO 17
<211> LENGTH: 592
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 17

agcaggttca gtcagacgtg taaacgacgc catgatgtat acgaactcat atagggcgat 60

tggcctttag atgcatgttg acggcccgca gtgtgatatt cgcagatcgc tttttttttt 120

ttttaggcat ggtgcgcgat gagctgatag cgatgatgaa gaccaagacc accaaaggaa 180

gattcttcag agcaaaagct acggagacag aaccagagga ctcaaagccg gaatccattg 240

gtgaggtacc tgcaaatgtg tgatggacta actaagaagg ctccttgaga ggacccatta 300

agcacagtgt ttttaagtcc caaattctgt tgcaattccg ttgaaaatca tttttacgat 360

tttaggtatg atgtgtgcaa ttttaaagtt ggaattattg tgggcaaagg ctataagtga 420

ttgtctaatc catttaattt attatctttt gactaagagc atatctaggc tggaagaaat 480

tagggcacat taatgtaagt tttgaatttg aacattctgg gttttgcaat gcaaaacacc 540

acaaatattt tataatgtta gaggtgtact ttttctggcc aaaaaaaaaa aa 592

<210> SEQ ID NO 18
<211> LENGTH: 204
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 18

ggtactccac caataatact tgtctgttct tgcttccctg ctgatccact aagcagatta 60

tttctgtcca ccccacttta gagtctcagt ttgtaaagca ctccctagga gctaaactca 120

tttccaatgg attaaagcac tccataggag ctaaactcat ttccaaggga tttttgtcca 180

tttctctgtg ctaaaaaaaa aaaa 204

<210> SEQ ID NO 19
<211> LENGTH: 347
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 19

atgtatacat atatgtggta ctccacacac tcaaataaca gcatcacaat caaaacaaga 60

aggcggccag aaagctttaa aatgctaagc ctacaggtaa tattcacaac tgcattaagc 120

accccgcttc ctagttctga agaagccaga aagctttaaa atgctaagcc tacaggtaat 180

attcacaact gcattaagca ccccgcttcc tagtaggcta gtactaggac taggaccgca 240

ttaccagttc ccttatcttc tactcatcct ctacaggaaa aactatgact aaaactgcat 300

taccagttcc cttatcttct caactcgtcc tctacaaaaa aaaaaaa 347

<210> SEQ ID NO 20
<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 20

ggtaatttcc acccaccacg ggctttttca attaacccat ttctaccact ccacattagg 60

gttctaagtt ttgtgactca cccccaattt cgctgatatt ttgcattgca gcttgtttat 120

ctacaggaaa tggctaatca gtactttcag aatttggttg cttctgtaca ggaaatggat 180

aatcaatcag tacttctata cttaagttgc ttacgcgggg atcagagcct tacttcagaa 240

aattgaatac attttcttct ttgtgtatgt atcaggcatg gaattatatg tagcatgcca 300

tggaatgcgt atttactaga ttatctttta atttaataca tatgttgctt actaatttgt 360

ccacaaaaaa aaaaaa 376

<210> SEQ ID NO 21
<211> LENGTH: 332
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 21

ggtactccac acactcaaac aacagcatca caatcaaaac aagaaggcgg ccagaaagct 60

ttaaaatgct aagcctacag gtaatattca caactgcatt aagcaccccg cttcctagtt 120

ctgaagaagg ccagaaagct ttaaaatgct aagcctacag gtaatattca caactgcatt 180

aagcaccccg cttcctagta ggctagtact aggactagga ccgcattacc agttccctta 240

tcttctactc atcctctaca ggaaaaacta ggactaaaac tgcattacca gttcccttat 300

cttctcaact cgtcctctac aaaaaaaaaa aa 332

<210> SEQ ID NO 22
<211> LENGTH: 238
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 22

ggtactccac tattagattg atgcaagacc aactgatcat ggctagggtg tattcaagca 60

tttcccaggc taggaataat cttgatttat accatgaatt gatgcttcgt attaaagaat 120

gtcaacgtac attgggtgag actaatgccg attctgatct acctcaaagg taataatttt 180

tgcattagct gcttctaaat caagagtagt aagtgcttcc atttgcaaaa aaaaaaaa 238

<210> SEQ ID NO 23
<211> LENGTH: 170
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 23

ggtactccac aaggcatata tgggcaattg attttgccta gcccaaattc ctattcaagc 60

ttgcgtattt ctaaaagatg cactattttt tgtccgagtg taggttttga attcattgta 120

acattcagca atattaattc aggggtagca tttctggcaa aaaaaaaaaa 170

<210> SEQ ID NO 24
<211> LENGTH: 152
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 24

ttttttttttt ttagggtaga aaaccatgct tcactaacaa ggtataaaat tacaatataa 60

ttctgggtgt aaacgacctg atagatgatc tgcaagtgcc aggaggcaat atctagcaga 120

atacgtacaa attaaattgc caaaaaaaaa aa 152

<210> SEQ ID NO 25
<211> LENGTH: 197
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 25

ggtactccac caatgatcac ccatgtccat ttggttaatt caatgtcaag atttagtagt 60

tccgtattcc cttgggtaag ctgtaatggt ccatttggga acagtccatg tttgggacac 120

aagttcaata gagatgtcat ccataaatat gggtatgaat ctcttccttc cctctccgcc 180

caataataaa aaaaaaa 197

<210> SEQ ID NO 26
<211> LENGTH: 199
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 26

ttttttttttt ttagtagcaa tagcaatcca ttttagggat ctgcagatca gtgactaagt 60

gacccctacc cccaaaggat taattgtact ttggcttaac cacaaaacct gattcaaaaa 120

atgtgaagtt tttacccatt aaattaattc ccaaaagtaa ctacaaattc cagagtacat 180

ttttacccaa aaaaaaaaa 199

<210> SEQ ID NO 27
<211> LENGTH: 455
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 27

ggtactccac tatacaatat caaggcatat ctgccggttg ttgaatcatt cggattctca 60

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agcactctcc gtgccgcaac ttctggccag gctttccctc aatgtgtgtt tgaccactgg 120

gatatgatgg gatctgatcc attggaacct ggttcccaag ctgggcagct tgtgactgat 180

atccgtaaga ggaagggtct taaggagagt atgactccct tgtcagagtt cgaagacaag 240

ctgtagagct ttgctatgtt tgcatgtcgg atgctgtcaa gattgaggaa cctccgagta 300

ttaaaacaca gttttgtgtg ctaggactat ttaaatttat gctattcacg tatttttgtg 360

atctgttatt tatgttattc acgtattttt gattggaaaa tacttttttac aagtcatcca 420

ttaatctttt aaatgttaca taattctctc ttgtc 455

<210> SEQ ID NO 28
<211> LENGTH: 93
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 28

aagcttggta ccgagctcgg atccactagt aacggccgcc agtgtgctgg aattcggctt 60

ggtactccac tatacaacat caaggcatat ctg 93

<210> SEQ ID NO 29
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 29

cttttcttcg tgcttttcgt ggagtacc 28

<210> SEQ ID NO 30
<211> LENGTH: 156
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 30

ggtactccac aaagtgagat gagtgatatg aggtcaaaca cgtaaatgac aatagctatt 60

atttccccac ttgtttgtgg ctgtgtatat tatacttcat tgtcaggact tttgtatggt 120

tgaagttgca aggttttggc aaaaaaaaaa aaaaaa 156

<210> SEQ ID NO 31
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 31

ggtactccac ctccagctgc ttatccaagt actacggata gttcatactc ctattatgct 60

tctgccaagt gaaccagaag gcttctgttt ctacactagc aaactgatag ctcgagcatt 120

ctcatttact aaggatgata attcaaaatt gtaacattgc aaacatcagc aaacatcagc 180

atcaactctg ttactattac aagcaatgga tgcgtcgctg atgctgcggg agagtaaatt 240

tttagtttac tgcggttggt aattgagtag gttgacttac atttctgttg taaagccgtt 300

gtcgggcatt gtttatctgg ccgagttagc gccaggaagc taaatgtacc aaatatttat 360

ttttatttta ttaagaatat aaaatttagt cgtcttctgc tgcccaaaaa aaaaaaaaaa 420

a 421

<210> SEQ ID NO 32
<211> LENGTH: 163
<212> TYPE: DNA

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<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 32

atggccatgg acttatgact ttcaaaaccc taaaacctat ctacaacttt ccacgctgag 60

attttccgag gaaggcattc taagccattc ccaccgtact ttaataaaat aaaaacaaga 120

agatagtaaa gctaagctac aaccttccgc caaaaaaaaa aaa 163

<210> SEQ ID NO 33
<211> LENGTH: 554
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 33

gaccgcttgt aggaacacta gcagattccg gaacataggt actttgaaca tctttcactc 60

ctcaccatat gaatagtgag tcgatggcgg ccttaacagt cgagcatgct ttgatttcgt 120

ctctctctct agtgaccgaa atcaatctca ttatatatgt cattatgcat tcattcccac 180

ttcctaactt tcattattgt tcaaaacttc gccttcctga aaatgctata atagtagggg 240

aatattgaaa aacttccgcc aagctaaaaa ggcacttaaa gcacctggat ttgaaccagg 300

atttcccacc ccgatgaggg ggggtgtctt tccattgaga cgatgcctta ctcggcagac 360

cctgtggggg tctttatagg tgacttaata cttaagtata ggacttaaga gagaggaagc 420

gaccgcctct ctgatcaagc ctttacgtgc gacgtgccca ggtaaaggct gatctcacca 480

aataattcag agaaagaaga tgactccaca gtagcgaaac tcctacattg tcttacatat 540

cgtaacaagc ggtc 554

<210> SEQ ID NO 34
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 34

gaccgcttgt gcctggtgtc caaactagga cgccttagtt ttcctaagaa ggaaacccag 60

gcgttgactt gaggcagact tgtgcttctg ggtactctca ttcactgcgt gaccttgaga 120

aagggacttt acctccagga tcctcaaact tcttctctgt aaaatgagca ttgtaataat 180

tatatcccag gcttatgttg ggaatattca ataaatgctc ccttcattct ttaaaaaata 240

agtaaagaca gcctgaatgg gagccacgtt ctcattcttc tttctctatg caaaatgtat 300

tgtgtaatgt ttgtgtacta gtagttcaag agcaaataag tagttggtta atggctaaca 360

tatttcttaa atttgtaact gttaagataa acattgaaca aggaaaaaga ttcgtaactg 420

aaatgtaaag tcatttgacc ctggatagtc aatgacaatc ttattcacag tgtaataagt 480

aattcataac gagatgatta ttatgaaatt atcaatagcc tgctatatca ctttatgttt 540

atgatccaca agcggtc 557

<210> SEQ ID NO 35
<211> LENGTH: 373
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 35

gaccgcttgt ggaagaaaag aaagaatctc tttcggattc aataggcggt atgggagagt 60

ctgctactgc ctcttggatt ccaggaatcc tagagctggg agtatgagtt ggagatgatg 120

aaggtgtctc ttacctattt cttgaagtgg atggagttgt gaaaatcgaa cttctagctt 180

-continued

cagctaaaaa ccttccccta gaatctcttg ctctatgcat atcattttta ttttttcttt 240

caagataggg taataattct ctttctgatc ttccaggtca ctctaggtgc aagaagagag 300

catagtcaag gaactattaa accaataact ttctcttttc tgatcctcca gttcactcta 360

ggtacaagcg gtc 373

<210> SEQ ID NO 36
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 36

gaccgcttgt gcaaagtaga taccgtcctg ttccggtgaa ttgaagtaca ttttcaaaat 60

gcgctactat gacattttat aggatgtctg agtgtaaaat aatggtactg gttgttgcaa 120

agaatctgat gtttggatgt atggaactat aaatagatgt tattttctga tccagaaggc 180

tttccttacc aactgatttc atcttcagaa actaaaagct cttgaacttg tgtagatggg 240

gcttggtcat tgtagtttaa atgcattatg tagtggcaaa aaaaaaaagt tatagcctac 300

gtttcaaatg gatttgctcg acaatcaaat gaattacaat tgaatattca tgtataccca 360

aattttaaat gtagaatgac atcatcaatg tagacaaaca ccactgtgct tgtccttgat 420

atcctctttc accatataat tggtggctta ctcaaagtca ctatctgatg caactacaag 480

cggtc 485

<210> SEQ ID NO 37
<211> LENGTH: 500
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 37

gaccgcttgt tcaatgcaga atctcgaaga gatgtcttgg acaaatactg aactggcacg 60

attggtgtag tgcggttcaa aaggcgctcc agattcgtct ggaacgaatc ttcatacgct 120

gaacaattag acatcttgta cgcaagagaa ttacgatcgg ccatataaaa accccaaaga 180

gaagaaagtg tttcgaaatt ctcccagaaa acagtcttat gccaccgatt tgtcttttca 240

acatgcattt gcaatgaagt ctttggattc ttactgtgag tgctgatcag caacggattt 300

tcgatctgta tagctctgcc gattcctggt taaagcagct aagagttagg catccagatt 360

ttgagttttt tgcatctcac aatgtttgaa tacatttcaa atccattgtt ggagtaacct 420

aacaacaact gtactcttct tcctatttct gaagccctct gccagtttaa ggcagagaac 480

tgagttatct acaagcggtc 500

<210> SEQ ID NO 38
<211> LENGTH: 398
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 38

gaccgcttgt ataataaagt ggtaccgcgt cctgcaaaca gggttctctt gccatcctgc 60

tacaaccctg cagtggtcgc agtagagaga atcggagcaa cgaacgtttt cccgaatata 120

tggagcggga ggaagagttt tcttgctgat gatccaatcg gagtcgaact gccaccgctg 180

gatgaagggc ggcgaggaaa tcttgggggg cagaggcccg tcggcgtagg aaataagaaa 240

cgatttgata tggaacgaaa gggcccgtcc agggttcgat ccccggcagg gcagccagcc 300

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ccgaactaaa caaaacaata agaacaaaca gcaaagtaaa agaaagcacc agaagaaaca 360

gcagcagacg aagagtaagg agctgcccac aagcggtc 398

<210> SEQ ID NO 39
<211> LENGTH: 179
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 39

gaccgcttgt aatccacagc attttcaata acttcctgag gtgacatcca cctccactca 60

gaaaactcgg ctgcatctgt cccatcacca gctagattga tctcactctc gtctcctcta 120

aattttagga ggaaccattt ctgtgcttga cctttccatt cgcctcccca caagcggtc 179

<210> SEQ ID NO 40
<211> LENGTH: 221
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 40

gaccgcttgt atataatgtg aagacacaat aaaattttgt ccaacaaagc aaccaaacga 60

ccaaaaattt agctgtgaca tcaaaaagct caacccctac aatgaatgta accttaatct 120

agaaaattga tccatgatct ccactgaatt ttctcgttca tcctgaagaa tgagaaactt 180

aaatgtaccc gattccctca accaagcccc cacaagcggt c 221

<210> SEQ ID NO 41
<211> LENGTH: 473
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 41

gaccgcttgt aatccacagc attttcaata acttcctgag gtgacatcca cctccactca 60

gaaaactcgg ctgcatctgt cccatcacca gctagattga tctcactctc gtctcctcta 120

aattttagga ggaacctgta attggtaggg gcttgtcata aatgatcaag acgacccgca 180

tcgtgatgcc aagcttagtc tttctactta ctgtctatgt aatggtcacg ggcccttctt 240

atgtttatgt ctctttgaaa tggacgattt ttttgtttta ggtattcagt ttctgaagct 300

gttttggtag taaactgggc tcaatcattt ctgttgcttg aactttccat tcgcctcccc 360

cacaagcgtc agccgaattc tgcagatatc catcacctgg gggggccgct cgaacatgca 420

tctagaaggc caatccccta tatgaattct attaaatccc tggcctcgtt tta 473

<210> SEQ ID NO 42
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 42

ggtgcgatcc agaaaactat catctctcac tgctcgtgaa caaaatgctg gttcatagcc 60

atcactaagg ctaaggtact atccagccaa actgatctca aataataatt tcataagctt 120

aaataaatag tccagccagt agatggagcc aaaaagccat agaagcttca aatacttgtg 180

gtatcaatct ctcctctgtt aagggaggta tcagatcaga agcactaatc aaatgcatac 240

ataaatgcag tagactgcaa taaaacaaaa tctgcagata gcaacagagc gcttaacgaa 300

cggaaaagag tttaacttga tctatcacag gatcgcacc 339

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<210> SEQ ID NO 43
<211> LENGTH: 303
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 43

ggtgcgatcc acaatagttc gtacgagcga cgtctatctg gttaatcaga acacatatct 60

aatttggaaa tttgtgggca taaagctcca cagtgtaggt gggctaatcc catgaaacat 120

tactcttcaa aacatcatac aactgaggtg gaaattgcaa aagattatta ctggatgctg 180

atctgggact aaggtggtgg ccattggtaa tgttgtgttt cagaaatata tcttcatgat 240

gatcagtagt tgcatctggt tggaagaatg ataaattctg gtaatttgtc ttgggatcgc 300

acc 303

<210> SEQ ID NO 44
<211> LENGTH: 274
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 44

ggtgcgatcc aactagaaga atataaagaa aaattacgga ctaccagaaa acatcacatc 60

acagtgtatt gcattctcaa taatcagaac tgtactggct aatatcgctg tgcctgtcgt 120

ttcattttcc tgtcatccgc atagggcccc tcattttccc tatcttgcag aaatccaaga 180

aatgcaagaa aaccaaaaag gaagaaaccc ccagaggaag agtccgaaga ggatatgggt 240

gtcagtcttt ttgactagat tggaggatcg cacc 274

<210> SEQ ID NO 45
<211> LENGTH: 269
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 45

ggtgcgatcc cagaacattt cagacagatt aaaacaagat ctagtcaatt cctacaaggg 60

aaacttttgt caagatccgg atccagattt tcctcaagta aaactaatct cattaaatcc 120

aagccaatct ctagcaaaat tcaaacactt tttattaaat ccaagccata tatctggcaa 180

attcaccgaa atatgtacaa tcgcagcgca ttgcttggct tgcgacagaa accatattcg 240

cacgtcttca taaggctttg gatcgcacc 269

<210> SEQ ID NO 46
<211> LENGTH: 240
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 46

ggtgcgatcc aacaacacag cttcacactt actccatcct ctggaactct catcagattg 60

tgttcttcgt agaccaagtt cctgtgagag tccacaggca cactgaggct acaagcgatg 120

tgttccctaa agaacagggg atgtacatgt tttccagcat ttggaatgca gacgactggg 180

caaccagggg tgggcttggg aagacaaact ggactgccgc tccattcagc ggatcgcacc 240

<210> SEQ ID NO 47
<211> LENGTH: 242
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 47

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ggtgcgatcc caacaccaag tgagaatgaa gcaatataaa tcagcagact cactaaagcc 60

aaaacagtga aaaatgtttc atattgggaa tctgctccag aatgagcctt caagtaaaat 120

gacaaactaa cgaggaagag acatacggcc atgcccccag atgagaccat gaggaggaga 180

cgtcgtccgg ctttatccat gagccataca gcaactgcag tcatgatgac ctggatcgca 240

cc 242

<210> SEQ ID NO 48
<211> LENGTH: 213
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 48

ggtgcgatcc aggaaatcat caaaggggag cacatccaat gtgcaaaata agatcatcat 60

gcagcaagat ctctgaaata taagctctgt aagaccaatc tgaagtgctg atgatcaata 120

tgaactgaaa catcatgcca caatgggctg gtacttgtgc aaaattctct ggcatgtgat 180

gagaatcaca tggttacctc tttggatcgc acc 213

<210> SEQ ID NO 49
<211> LENGTH: 235
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 49

ggtgcgatcc aaagagcctt cttgcagaca atccgtgaaa acatggctat acaataaatt 60

cccagtttgg aattctaaat aaaactgttc aatatttgaa ggcctctgat atcacagaga 120

ctgatattag aatggaagca tgtagcaacc ctagaagctt tcgcataaag ataccagatt 180

aattcataag aaggatctct cgttcaccag tcacatatca cagtcggatc gcacc 235

<210> SEQ ID NO 50
<211> LENGTH: 216
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 50

ggtgcgatcc gttagatgag ctgccaagta tggaattatt gacatttttg gacgggttat 60

gggcagaggg atgtgccaag ctgaagaaga taccggggtt ggagcaagcc acaaaacttc 120

gagagttaga tgttagtggg tgccctcagt tagatgagct gccaagtatg gaattattga 180

catctttgga cggcttgtgg gcaaagggat cgcacc 216

<210> SEQ ID NO 51
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 51

ggtgcgatcc acatagtttg aatgcaagga aattgcacat acttcgtggg gaatttcgat 60

ggcaaatcag tccaggtaaa tgacttctca acataggtcc aaaactcttt catagaccag 120

atcttgaccg tgttgtccat gccacagctt gcaatacgat atacatctga aggatgaaaa 180

tctacactga gaacttcatt gcgatgtccc ccagctccag caaatatcaa aatgcatatt 240

ccagtttgaa cattccagag tcgtacagat tcatctttgc tagcagataa aataagggaa 300

ggtttcagtt gcttgggtcc ttatttcatt cacagaactc catggccaac gaaactctta 360

tggacttttc atttgcacat ccattctcga attatacatt gtgaccgcag ccactaataa 420

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tggggaacat cactcgcctg cccacttatg tgttaaagaa tc 462

<210> SEQ ID NO 52
<211> LENGTH: 246
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 52

ggtgcgatcc cctccattta ccatggtata ctgttccaaa ggttccagag cctagctctt 60

tcaattcttc aaggtcagca ttctttatta tctggaaact tcgctagctg tgtctataat 120

cacgaaaccc agacggggaa ctaataggcg atgaagtttc tcttatccat aaccgttgca 180

aagatcttac acggagtttt ctcttcttct gcgtggcttt tctttcccgt attctcggat 240

cgcacc 246

<210> SEQ ID NO 53
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 53

ggtgcgatcc atacatgcga gggcgcatga gagactacca caaatcctac atacctccat 60

tcacccctgg atcggttata caaggatttg gggtggctaa agtgatactc tcaaatcacc 120

cagacttcag agagggtgac tttgtatctg gtactatagg atgggaagag tacagcataa 180

taccaaaagg gagtaactta agaaagatca aatatacgga cgtaccactt tcatattttg 240

tgggtgtttt aagaatgccc gggtttactg cttatgctgg attctttgaa gtttgctctc 300

ctaaaaaggg ggagcatgtt tttgtctctg ccgcttcagg agctgttggc cagcttgttg 360

ggcactttgc aaagttgatg ggttgctatg ttgttaggga gcgcgggtaa caaacagaag 420

gctgatctgc tgaaacataa aatgggcttt gatgatgatc tccaccataa cgaggagcat 480

gacttcgatg tggctttaaa aaggcatttt ccagatggga ttgcacc 527

<210> SEQ ID NO 54
<211> LENGTH: 273
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 54

ggtgcgatcg aactgaatga atgacgttgc caagctatgt ttgggaatta aaacttgaat 60

gccgttattc tctccttttt ccaaaagggc cttttctgcc agaaaacctt aaatttctga 120

ctggtttcca agtccaattt ttaaaatatg gattggttta ccattgaagg caccaccatg 180

ctctgaaagt tatggactgc acttgcccca gtgctatatt tagtccagat agcgcttgtg 240

tctctaaatg catctccctg ctcggatatc acc 273

<210> SEQ ID NO 55
<211> LENGTH: 220
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 55

ggtgcgatcc gaacagaggg agcagatttt gcccttgcaa gtattcacaa cattagagaa 60

gccctgccag agatatggga ggaagaagat gcagagaaca ccaaaaatgt tgtgggatca 120

agaggagcgg atgcaactat agaaactgtt gtcacggcat aagccatcgc ctcattgaat 180

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gagggaatgg aggactagac aaatcccttt ggatcgcacc 220

<210> SEQ ID NO 56
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 56

ggtgcgatcc gattgggcag ctgcagcctt gggaagcttt agaatcaaat tgcactcatc 60

ctccaggagg tattgagaag tcaatttctc aaggtctaca gtgacagaag gaaccatctt 120

gacaatctta tcaggtttcc tgctctggtt aaacacttca actttgacag gacgagagaa 180

tgtgactaat tcatcttctt catcagactc tacatcttcc tgtttcaaga aacaaagata 240

ctgatcatca ctagggcaag aattgatgat tttgatatct ctggagaagc cagtgtttac 300

attggtttgc ttcatggcca ccagtctatg gcataaagct ttcccgaaag ggtacttggc 360

agatttaaca gagcccaacg ttatatttaa ggcccatctc tttgctctca aaatttttct 420

tgcatcctct ggagaatata aaaccccttg gtgtctcttt ccacaaacac cttctcattg 480

atc 483

<210> SEQ ID NO 57
<211> LENGTH: 472
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 57

ggtgcgatcc aactgagaag ggtgtttggt ggaaagatga caccaagtgg gttctatatt 60

ctccagagga tgcaagaaaa attttgagag aaagaagatg ggcccttaaa tataacgtgg 120

ggttctgtta aatctgccaa gtacccttca ggaaagttta tgccatagac ttggtggcca 180

tgaagcaaac caatgtaaac actggttctc cagagatatc aaaatcatca attcttgccc 240

tagtgatgat caggaagatg tagagtctga tgaagaagat gaattagtca cattctctcg 300

tcctgtcaaa gttgaagtgc ttaaccagag caggaaacct gataagattg tcaagatggt 360

tccttctgtc actgtagacc ttgagaaatt gacttctcaa tacctcctgg aggatgagtg 420

caatttgatt ctaaagcttc ccaaggctgc agctgcccaa tcggatcgca cc 472

<210> SEQ ID NO 58
<211> LENGTH: 246
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 58

ggtgcgatcc atgtagtgcc aacttacgag atcactaact ttaaaactat catgcaattg 60

gccaatagaa gcgacacttg ctgtgccaaa gtatcgatag gctactcccg atggctcaat 120

catatatagt tggggcccat ctctatcata acctccaagg ataactccag atccaaaagg 180

ccttaaccac caatatagtg tgcacaaatg cacataactg gcaacacgtt cacaaagttc 240

cttaat 246

<210> SEQ ID NO 59
<211> LENGTH: 255
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 59

ggtgcgatcc catgggatag ttgcaagaca cacaaatttg ttgtgaaaga agagagacac 60

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gcacagacaa ccatatgatc ttttttttt ttttttttt ttttttttt ttttttttag 120

caaaattcaa acacttttta ttaaatccaa gccatatatc tggcaaattc accgaaatat 180

gtacaatcgc agcgcattgc ttggcttgcg acagaaacca tattcgcacg tcttcataag 240

gctttggatc gcacc 255

<210> SEQ ID NO 60
<211> LENGTH: 368
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 60

ggtgcgatcc cactgtagtt gtccttgttg agcatagttc aagctgttct gattccacca 60

gttagtggcc caacactgcg aggtgctgcc atttccattc cattcacaga cgtcagtgtt 120

gaaattcata taggaagcca caaagggtga ggaagaccaa tctattttca ctcgcccccc 180

ttgagttgcc cactggtctc cgctccatat gctagagaat actctcattg cctgctcatt 240

cggataggga acgcctatgt tttcattgtt tgcaaatact ctgattggca aaccatcaac 300

gaaaatcgca atttgctggg ggttccagag aatagagtaa ttgtggaaat ctgctgtagg 360

atcgcacc 368

<210> SEQ ID NO 61
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 61

ggtgcgatcc cacactccta accctattat atgtctcccg tccatggagt catagaagga 60

gtacgataat atgcccttca gccaagcgaa gtatgacttt agtatggcca ggcagcagta 120

tgaaagcaca tcttgtttct tccaggtcgg catgtatagt ctccggaggc taacaatgtc 180

acccaaagct aattgcgcaa acggaactcc tctgctgatc tcccgggaac ttaggcggaa 240

ccaccctgaa tccactattc tcaccgcgca tttcatccct ttggtgaacg ccgctgcctc 300

tggtagatac agagctggct tgtctccact ggaacccccc ttccggatcg cacc 354

<210> SEQ ID NO 62
<211> LENGTH: 364
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 62

ggtgcgatcc aaactgtggt tatcggtgga gagattaagc aatttattgg agtagcaagt 60

acgctgaatt aaggggtcc atcttcaagc aaaggttcct ttggatgact atgtgttctg 120

gaagtgttta tggatcaatc atctcataaa ttttggtaat atataacaga agattatggc 180

atccagttag gatggtagtt tcattgaggt atagtaaaaa ctacactagt cttgtgttgc 240

cacccacttt tcagagaagt caggaggtct ctttgtgaat cattgataac tttatgagtg 300

ggtacctaaa tgaaatattt gcatcttgag tatatactca attgatctta cttgtggatc 360

gcac 364

<210> SEQ ID NO 63
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 63

cttggtaccg agctcggatc cactagtaac ggccgccagt gtgctggaat ttacggctgc 60

gagaagacga cagaacacct atcataactt gaattctgat gcaaatcgga atttgccaaa 120

aacttggacg gaaatataat aggcaatatc atccccgcaa gtaacaaaaa aattgcatga 180

aagctcaaat cctatgtgct ttacaccttg actgcatact ttctcattgg aaaatacatc 240

tctttctttt tctgtctctc agtcttcaat gacgcctgat gcttggtaag gcgtcgcctg 300

atagcacgag tcttcttggg acgcaaatca agaggcaggt acttcttttt tttgtatgct 360

tctcttaatg cggatcgcac c 381

<210> SEQ ID NO 64
<211> LENGTH: 382
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 64

ggtgcgatcc aagattgtac ggcacaggca aatgctgttc tttttcttaa tcacgatgtg 60

cttgaagaat atgagcgccg atgtgaacag atccacaacc tggagttaaa attggaggaa 120

gacagagcag tgctgaatag gagcttggca gaaataaata gtcttaagga atcctggctt 180

cccacattga ggagtttggt taccagaatt aatgaaactt tcagccacaa ctttcaaggg 240

atggctgttg ctggagaagt tacactagat gaacatggca tggattttga caagttatgg 300

tattctaata aaagtcaagt tcaggcaaac tggacagttg caggtattga attgctcatc 360

atcagtctgg agggatcgca cc 382

<210> SEQ ID NO 65
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 65

ggtgcgatcc gagggaagcg atgtagtctt gccccaagcg acgaccatga tcccttattc 60

ttgggcaata tgtgcaagac gtggacaaat gaagcggtta aagggaagct tatggactat 120

ggaatagagg gtcttgaaga gctaactcta gtgggtgata ctcaaaatga aggaataagc 180

cgtggttttg catttatagc attttctacg cacatggatg cgatgaatgc atacaaacgc 240

cttcagaggc cagatgttat ttttggtgct gatcgaactg cgaatgtggc atttgcagag 300

ccactgcgtg agcctgacga agagatcatg gcccaggtta agtcagtgtt gttgatggga 360

tcgcacc 367

<210> SEQ ID NO 66
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 66

ggtgcgatcc agtcctgaaa atgtacttta ccatttgtat aatgatgtaa aaatcttggc 60

catagtctgg tcaaaccaga ctgtattgtt gctaaagtta tggaaattct ggccatattt 120

ttgtctaacc agactgtatt gttgccaaag ttatgggaat tccggctata tttttgtctt 180

cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaga tcatagggtt gtctgtgcgt 240

gtctctcttc ttacacaaca aatttgtgtg ttttgcaact atcccatggg atcgcacc 298

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<210> SEQ ID NO 67
<211> LENGTH: 425
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 67

ggtgcgatcc gctggaaggt gggcagctgg acatctggga attataagtc gaatgtcaat 60

tgctgggcca tctgggggat gagcaatagc atcggaggcc aagttcttct gcagccgggc 120

accaaatgcc atgtggaggt ctgaatctta gtttggaggt cgaagtttca atccccttgt 180

gtttactctg tttctggttt tatttgaata atttgagcaa tttaatgtgg gtccttagtg 240

cttctgtgga tcagattcta gggaacgcca tcctgataag taaagatccg agttttaatg 300

gagattcaat tctatcagaa ttccatggtg gtttaaattc ccttgtactg ttgatctacg 360

tcgctttgta tatcagtgtg tgttaagatt ttctcagaat ccacagcttt gttatggatc 420

gcacc 425

<210> SEQ ID NO 68
<211> LENGTH: 335
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 68

ggtgcgatcc aagcacttac gactcccaac aaggacggga aactctaaaa tcggaaaaat 60

atcatatact gaggcatcaa ctttgttgat aaaactttaa acaagaacaa tatttgcagc 120

atattagccc acatgccata atgacaaaca aatatgagaa cactgcctac aggtttgcca 180

aaagcatggc cctcactttt gccctgaggt catcaggagc ttctgaggct cgagaaggag 240

aaaaagattg tgtcacttca ggagctgagg cctccacatc ttttaatgat ttcgcagcag 300

gcctctcttt aatgttttct ttagaggatc gcacc 335

<210> SEQ ID NO 69
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 69

ggtgcgatcc aaggtacgag cgaacaagtt tcttcagcaa gccacctgga actttccatg 60

agtccaaaac aagttgaaga aggcttcttt ggctactttt aagatgctga agtgattgtg 120

ctcgcctctt gcacagttca accgcaataa cattgggttt tacaaaaccg attacctgtt 180

taacctgctg tgcactcttt ttcgaaacat gacaagttcc aacaagataa acttcggccc 240

cattctcgcc attccgcaaa taaaccacgc tctcatcttc tgttatcgaa ctcgagtgca 300

tgccacgacg ctcaattgca ggattccaac cccggacttg cgaatggtgc aaagcgatgc 360

ccgttcgtct cagcgatact gctaaagatc ggcagacccg aaccagtttg atgcttccat 420

tgccttaaac atccagagtt ttccttcgac cttaaaccct aacaagatta ctgatttctg 480

gtccggatgt tcactgtctg ttatacttct cacaaatctg tcacactcct gataatcttc 540

ggtattgaac ttcattgaat tgaattttcc ttctcattgg aattcaattg taccttgtaa 600

atgtctggat cctacactat accaatattt acaggtctga gtattttgcc tgtagtataa 660

ttatctttcc ttcggtctcg tgtttccgta ttattcgtgt aggatcgcac c 711

<210> SEQ ID NO 70
<211> LENGTH: 622
<212> TYPE: DNA

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<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 70

ggtgcgatcc cgggggagg ttgatgttct gagagaatca atgaagggat ttcagctgag 60

cttgcctttt tgaagacgga atgcgaacaa ccagtcattt gcaatagcga gaattctctt 120

aagccactgc ctgctgggga ggcgagttct gattccggtg attgcatcac tcaacggcag 180

cagcagcggc agaaccttta gtttcccatg acaggtctct ctgtacaagt atcttcctgt 240

tatgatctaa ttccgggttg ttcgattatc gtgatgtctc ctgtattgac atattagcag 300

aatattacca tgatacgatg ttaagtggca tggtttatgc cctgcatgtt atgttatgga 360

ggaggtgagg catgtggcgc tcatgggagg gcccacatgg tccatggacg tcttattaaa 420

cgcatagtcg tgaatgaaaa tagttcaata cattcaaaat tccaacacaa tttcattaca 480

atggaagtga cttcgacttg aatgttcatt gaagcatttg catgcacaaa caaagtatac 540

tagattagaa gaaaattgca aaaaaggaca ttgtgccctt cttagtgaat atataaagat 600

gttcttcatg ctggatcgca cc 622

<210> SEQ ID NO 71
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 71

ggtgcgatcc caatagccaa tattgcctcc aagatagcct agactgcctt ttgcatagtt 60

ctagaagcca gtcacccaac ctcccaaaag aaattgcgca atctttccca tcagtttccc 120

gggtatgtgt tctgtcattc cccgaatttt ctttggtttt cactaataga tttctttcca 180

tgcacattgc ttgtctccag atcttttagg tgttcatcca tctcttagta gtactagatc 240

gatggcttcc aagagaacag gatcatatga cactgttgga aatgtagctg gagcagcagt 300

tgagcaagtg tcctctagtc tatctatcta tgaaagatac acattgtttc tagacatgga 360

tatcaaattg aaattgccag aagtccatga aacatttgcc gccttttgaa gaaaggctcc 420

aaactgtcag ggttcgttga acatcacatg ttctcgctgt ctgatccccc c 471

<210> SEQ ID NO 72
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 72

ggtgcgatcc tcagggtaat ggcctggctg aatcaagtaa caagaatctt ataaccatta 60

tctaagaaga tagtaggaga taacaagcgg tcttgggaca acaaaatcaa gtgcgctttg 120

tgggcagata ggataactaa aaagaaagcc actggtaaaa gtccctttga acttgtctat 180

ggcatggatt tgacattaca tgcccatctt aaattactag cttaccaact ccttcaacat 240

ttttctagtg ataaaggtgt tgtccaaaac atggttgatc aaattgtgca gttggatgaa 300

atccgcagga aagattttga tagtgcaaaa atcagtctac cattaagaaa atctttgaca 360

aatcttctcg gtctagatat ttacaggttg gagatatggt tttactatgg attccacc 418

<210> SEQ ID NO 73
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 73

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ggtgcgatcc tgcaggctta gatagtttcg gcgctcctct gaaagaagca cgagtaggtg 60

tctccacatt aggttggcct gatcccttgc ctgcacttgc agcttgtctt acaacatctc 120

ctatgctttg atccaggctt ttcactgaca taacttcagg ggcttccttc tcccagggcc 180

gtgctgccat ccagcgttct agccagctcc atccccaatt tggcttgttt gggtcaattt 240

ccatcagcat aggatgagct gctcctcgtg tgcttttcaa tgactgatga gaatatgcgt 300

tatgccaatg ccctttctcg cttcatggct gcttcttgct tgctttgcaa actagcctca 360

atttcctctt tggattgcaa ctgtcatcca atcctttgct tccatactgg atccac 416

<210> SEQ ID NO 74
<211> LENGTH: 346
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 74

ggtgcgatcc caaatgaaca ttcaacattc gatcatgtca agcgctaaat gccttggcag 60

cttaaaagct agactccgca agtgaccctt ctgacttagt acacatatta agactcatca 120

agggtccaat tccatgaaaa gaaattttaa aacggttaca tattcacaag aacagcacga 180

gatttcccag atagtcaacc accaacttgc cctatcagcc caaatattac tcattccatg 240

ttaaaaatag caaatttcca gatagaatgt cgaaagagat cttcatgcac catatatgga 300

ctcttaaaac cagccaaaat ctatactgcc atgcttggat cgcacc 346

<210> SEQ ID NO 75
<211> LENGTH: 346
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 75

ggtgcgatcc tggagagaga agcaaaaagc ctaccatcta aatctacatt ctaaatcaga 60

tatctttact gtgaaaggaa ttgaatgctg cttcagatat cctacaagaa ttaagaagaa 120

aagaatgatc aactccaaat caggcagatg gctcagaatt tcccgcagct tcattttcga 180

cggcctccac aacaccaacc tcggcaggac gtattactct gccatgaagt gtatagccag 240

gcttcaaaac cacagccaca ctgccaggct gcttactagc atcttgaact tgagatactg 300

ccatgttgca tatgaggatc aaactcttca tttattggat cgcacc 346

<210> SEQ ID NO 76
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 76

ggtgcgatcc ccagaggtta ttttgggttc aaagtattct acaccagttg acatgtggtc 60

atttgcttgc ataatttttg aactggctac aggtgatatg ttatttgatc ctcagagtgc 120

agaaggttat gaccgcgatg aggaccacct tgccctgatg atggagcttc ttggaaaaat 180

acctcgtaag atcgccttag gtgggagcta ttcacgggaa ctttttgaca ggcatgggga 240

tttaaagcac attagacggc ttcggtattg gcccttggat cgcacc 286

<210> SEQ ID NO 77
<211> LENGTH: 395
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 77

ggtgcgatcc taaactgtat gtctccacaa ttgtcttcaa tatagaagca gctacgcccc 60

tcctaagtca tcataagtta aaaacttcat ctttccaata caattaaact atctagctta 120

tcagtttgga atagagatac aaaattacag atagattagc gaaactgtgc cacaaaacct 180

cttcaaaatt agaagcatga ttgtctacaa ctccacttca aaaaggagct gaaccagtcc 240

ttcgaagggt gtgctttggt tgtggtggag gtacagaagg cagcaatttc tccaagaact 300

gctgtttttt tagcctctca ttctcctctt taagctgcat cacttcattc tctagctcat 360

ttgtgtatgc ctgctttctt gccctggatc gcacc 395

<210> SEQ ID NO 78
<211> LENGTH: 308
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 78

ggtgcgatcc gagtgatggc acaaagaaaa gcaatgatag aaaacaaaga acaggtagct 60

cagaaggttc agcaacttag agagtcaact tcgagttaag gagggcggga gcaattggca 120

gattcttcca aatttgtcaa gatctcttgg catgagatga ccttatagga tgttaaggag 180

caagaggatt ctaggaataa tgccaaggat aataagacta aaaggatgct tcaagaccag 240

gtggcaagga aggcttctaa ttcaaaggga gttagcaacg gcaacagatg caattctagg 300

atcgcacc 308

<210> SEQ ID NO 79
<211> LENGTH: 307
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 79

ggtgcgatcc tagaattgca tctgttgccg ttgctactcc ctttgaatta gaagccttcc 60

ttgccacctg gtcttgaagc atccttttag tcttattatc cttggcatta ttcctagaat 120

cctcttgctc cttaacatcc tataaggtca tctcatgcca agagatcttg acaaatttgg 180

aagaatctgc caattgctcc cgccctcctt aactcgaagt tgactctcta agttgctgaa 240

ccttctgagc tacctgttct ttgttttcta tcattgcttt tctttgtgcc atcactcgga 300

tcgcacc 307

<210> SEQ ID NO 80
<211> LENGTH: 521
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (391)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (428)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (433)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (443)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (471)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (494)

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<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (497)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (512)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 80

atctagatca tcgatcttgt ccaaatttta actagtgaat agttttaaaa aaaagcaact 60

agcagaagag aacctaacca ctgacaaatt gcaaatactc tagaacacta ttcatcattt 120

tttgcgattc acgctggacc cacaagaacc ccttgagctg aactttcttt tcgttctccc 180

tccttttgga tcgcaccatc tagaccatcg atcttgtcca aattttaact agtgaatagt 240

tttaaaaaaa agcaactagc agaagagaac taaccactga caaattgcaa atactctaga 300

acactattca tcatttttg cgattcacgc tggaccacaa gaactcttga gctgaatttc 360

ttttcgtctc ctccttttgg attggacatc naatcctgca gccggggatt catattctta 420

acggcgcncg cgnggactcc atnccccata tgatcttttc atcctggcgc ntttaactct 480

gaagggaaac cggnttnccc ttatccctgg anatcccttc c 521

<210> SEQ ID NO 81
<211> LENGTH: 163
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 81

gtggagtgta aaggtcaacg tgccatccgg gtacaaacta ttgtagaaaa aatggcaaag 60

ttaggtctga aaatatccat ttggcctgct ctagttgtac agtacatgat tttgcactcg 120

cacaacaatg gactataatt attttcctgg caaaaaaaaa aaa 163

<210> SEQ ID NO 82
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (330)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (349)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (364)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (368)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (411)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (431)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (447)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (461)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (476)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (478)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base

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<222> LOCATION: (480)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 82

ggtgcgatcc aggacatgag gccgagtttg ccattgtgat atgattgagg aagtccagtc 60

ctaaaattag gtttatcttg atgtttgaca agagatatag aggggcatga tgattcattg 120

atctgtttgc agatctgtaa ctgcaaccat tctaatgaca taatagcgct attgtttggg 180

ttcgtgtgat gacataataa attgatttaa tttaataaca tctgttaatg caatggctgt 240

agctgcatca tcaccgtatc catcgaatgt tccatttttc caaatgtttg tttccaaaac 300

cagaacacca aaatgtcccc tgcgtttgtn ttgaaaaata ttgggcccnt actatactat 360

aatntttngg catactatac tataatgttt ctcccattcc ccccaaatga ntcctataca 420

atcctggccg nctttacact cctgacngga aacccggctt nccactaatc cctggncnan 480

cccttc 486

<210> SEQ ID NO 83
<211> LENGTH: 144
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 83

ggtgcgatcc gactgtgata tgtgactggt gaacgagaga tccttcttat gaattaatct 60

ggtatcttta tgcgaaagct tttagggttg ctacatgctc tcctcttttg tatgaatttc 120

cattctaata tcagtctctg tgat 144

<210> SEQ ID NO 84
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 84

ggggagtgtc aagggataag tggtaagcca ggtttccagt cagaagtgta aaggcggcca 60

gtgatgtaat agattcatat aggggaatgg agtcaccggg gtgcgccgtt ttagaatagt 120

ggatccccgg ctgcaggatt tgatggtgcg atcctgcccc tgataatttg gttgcaatgg 180

aaaatgcagt attaggtgcg agatgtaaag cccgcccgga gcggtgcatg aagtactgca 240

atatttgttg tagtaaatgt gctggttgtg ttcccagcgg tcactatggc aacaaggacg 300

agtgcccctg ctacagagat atgaagtccg cagccggcaa gcccaagtgt ccctgatctt 360

agcacttcag tccagtcgct cacttctttt attctttttt tttataaaag tgacgaggcc 420

gtttttcttg tacttggtgg ccatatgtag agcggtggct acttctcctg tgttaggaaa 480

tgttgcagta ctaataataa gaacttcttt ggcaaaaaaa aaaaa 525

<210> SEQ ID NO 85
<211> LENGTH: 543
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 85

gggtttcctt aagagttaaa ggcgcatgat gtatagaatc atatagggga tggattcccc 60

ccgggggcc tttcagaata gggattcccg gctgcaggat tgatagtgcg atccaagaca 120

cagtggagta ccacaatggg gatctggcca gtgctttgtg gctattcact gcagctgtat 180

taaaacagga agccgcaaat ggccagaagg ccattgaact tgctgagagc agactatcta 240

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aggatggctg gcctgaatat tatgatggga agcttggacg atatattgga aagcagtctc 300

gaaagtggca aacctggtca gttgctggat atcttgtagc caagatgatg cttgaagatc 360

catcccattt aggtatgata gcattggaag aggacaaaaa gatgaagccg tccctcactc 420

gatcagcttc ttggataatg taaaatgggg aaatcctaaa ctttcaggcc actcttgaat 480

gttttgtcac ttctgtatga caaatgaggc aattcatagt acatgttgtg caaaaaaaaa 540

aaa 543

<210> SEQ ID NO 86
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 86

ggtgcgatcc cagagaatat tagttcatgt gttgctctca ttttcttcaa tatgcagggc 60

aaccatttga atgaaattat tcctttcgaa tttcaaaaac ttaataggct aacttatcta 120

tctggagccg attttcattg acgagtaacc tgtaagctgg ccagcaaaag ccaacagatg 180

ttcagctcgt tggaaccagt tgaagattgt aatagagatg gtgaataatc gcggacggct 240

cggccaatgg aatatttgtt gcatcatcat caaggggta tgaattccaa agaacttgtt 300

gattgaaatt cccaagcaaa attctgtgaa atgaaaaatt tattgagacc attgggcaaa 360

aaaaaaaaaa 370

<210> SEQ ID NO 87
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 87

ggtgcgatcc aaagaacaca agatggagtt accacaatgg aggatcttgg ccagtgcttt 60

tgtggctatt cactgcagcc tgtattaaaa caggaaggcc gcaaatggcc agaagggcca 120

ttgaacttgc tgagagcaga ctatctaagg atggctggcc tgaatattat gatgggaagc 180

ttggacgata tattggaaag cagtctcgaa agtggcaaac ctggtcagtt gctggat 237

<210> SEQ ID NO 88
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (379)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (394)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (400)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (403)..(404)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (406)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (414)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (421)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (430)

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<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (433)..(434)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (444)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (450)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (454)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (463)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (470)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (476)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 88

ggtgcgatct gtgtggctct gaaacatccc ggctcccctc tgcactataa taatcccaaa 60

attaagtgaa cccaacagaa tttgctcata tctctacagt tattgcagac tgagcaaaac 120

cctcaaactc atgtgacctc tcaataggag cccacgccca agatttgtcc agcatgtaac 180

acacctgatc gccgccactg caagcacaac cgctcacaaa tatcttgtca caccacactg 240

ttgcgcaagt taacaatatt catgtctcca ggaaagaaat gccacacttc ccaacattct 300

ctttactatt atagaacttc cttgttgcta tggaaaaaat acattcccaa cgcagaaccc 360

caacgggggt tcccaatanc ccatttcccc cctntccaan ccnntntgaa tgcnccccat 420

nccctattgn atnntttaaa tccnggcgcn ttanctggaa ggnaacccgn ttcccn 476

<210> SEQ ID NO 89
<211> LENGTH: 364
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 89

gttttcccag tcaggacgtg taaaacgacg gccagggatt gtaatacgat tcactatagg 60

cgaattggag gtcgatccgt ataggtagtt ggatgatgaa cgggcaaaga aggcaaagga 120

gtacagtgat ggatcctgta attcctgttt cagaaaacag aaaatctgca atataaggat 180

ggctaagctt ttcagctatg aaaatatatg gtgcagtggc actcatatca gttgcagagt 240

tgtcaatata acttttgtga ataggaaagt tgtcctcttt tagagtgcag aaatcctgca 300

atataaggat ggctaagttt ttcagctata tgaaaatata tggtgcagtg gcaaaaaaaa 360

aaaa 364

<210> SEQ ID NO 90
<211> LENGTH: 170
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 90

ggtgcgatcc tacagagagc agcttgacga gggccaaaag gttaaggatg aagaatgacc 60

tcagctagta aggtttacag aagcagcaga ggcatcttaa ctgtttttat gttttggcaa 120

aagttgttgc gtcggttgtt taatccagga tttcagatgt attttgtaga 170

<210> SEQ ID NO 91

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<211> LENGTH: 210
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 91

attgtaatac gactcactat agggcgaatt ggagggtccg atcctgcgag accgagggtt 60

cattttcctt tagacaacga cgttcagtgg cgaccagagt ttcccaatca cttcagcgat 120

tctattcctt cgttgtaata aagcttaagg aatccatgct ttattccttg gaaggtttga 180

atatttatat ttattggcaa aaaaaaaaaa 210

<210> SEQ ID NO 92
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 92

aggtgaccgt caaaatgatt gcagaggact tagagaggga aaaccgttcc gatctggtga 60

agcaattgga tgaagcagct ctggaattga ttcccgtttc tgatgatatc gtacggctaa 120

gctcagctct tcaggcaatt ggcagagaat acgattcttc aaatgagatg acagatttta 180

agaaacttat agatgaacat atttccaagc ttgaagcgga ttcccctacg gtcacct 237

<210> SEQ ID NO 93
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 93

aggtgaccgt aaaatactat gagaaatgct ttcatcaggc accgctggta ggttttcttc 60

aagcttttca ttaggcaaaa gaggctccgt gagttgatcg ttaattctct ccttgaatgg 120

ccatattgac cagacactct gattagaaac tggaatacaa ctgcacatat agtcattctt 180

atatgattca tccttctgca cttcagcatc ctgcggcaac tcttcatccc gccatactgc 240

agaaaaatta tttgactctt gatcatgttg tagatgaatc ttcatgaatc ttctcatctt 300

gcattcttgt ctttatatct ttaggaaatt gcatctggta aaagtataaa tgcatcttca 360

ctggttgctt cagtttttgc atgctcctgt tcttcttgtt tacatgtgat ctaccaaatc 420

atctaatgta ttctctcaat gtcttgtgga cattctcctt cattccgaga ttaccaatca 480

tctacccgaa taaatgttgc cccgtcagca atgccgtttt ggtcc 525

<210> SEQ ID NO 94
<211> LENGTH: 437
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 94

aggtgaccgt agtaggcgtc cagaggctga caaaatccca ggcctgtgca aatctggaag 60

ccgcatgcag ggccgtggca ccttacactt gcggccttaa caaagtggcc cgcggcaccc 120

acttctacca gtgtgtttat attcttgtgc agccaacacc agaggttatg caggcgaatg 180

tgctggccaa gcgttgtttc ggcttgtccg caaaccctct cgagtcttac atgccgcata 240

tgagtcttgt gtatggcgat ttgcctgacg acgagaaaga gaaggccaag gttaaggcgc 300

agctaaattc gatgaactta tccgcaacac ggaattccaa gtctccagct tgtgcttgta 360

ctcgacagat ctgaaaataa tcctcactca tgcataagtg caaaatgtga tcttaacctg 420

ctctgaaaat tacataa 437

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<210> SEQ ID NO 95
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 95

aggtgaccgt ccacgagaat ttggcttcaa aaccctagga gagggatatg aacttgccaa 60

ggcacaactg acgcatgaac aagacgtaaa atgactcatt agacactgac atgataatga 120

aaaacctatg aatgatgata gactcagcta cttgatgaca tcgcccgcca tttggacatc 180

tttataagga gtttaagcaa accctagacc tactgcctag tgaccaactt ttgcttgacg 240

actcactgaa atgacaatat ttgaccttga cacttcaaaa tcactttgta ggaactcatt 300

tgatcactgg aggacggctg gaaagactga cactaacagg actttatata tgcacctcgt 360

ctatccgaac tt 372

<210> SEQ ID NO 96
<211> LENGTH: 442
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 96

aggtgaccgt aagcacaagt cgtcaaaatt atctctattc cggcagtaaa aacctatagc 60

taatgatgga tcaatagcac taagtggcag ctggcgtaca tcactgcaat gataagaacc 120

agtatcaacc cccatattat caggagatat ctccaccacc tgctgcacta catgtggatc 180

taagtacaga gcctgatcat cctgaacacc aacaatatac gttgaagctc caggctttcc 240

accagcaata ccaagacttt ggggaaatgt gaacgtttca cgaagtgatg gtacatacct 300

tgggttgatc ttctctacac caagaacaag cggcaccaaa atcaggatag gcacttggtc 360

ttccccttct ccattggacc actctgaaca cagcctcgca gcatcatcaa tgcagataac 420

tggagtccct ccacggtcac ct 442

<210> SEQ ID NO 97
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 97

aggtgaccgt gaatatggtg ggtatttgca gggcaagatt caggatgctg ctcccggagc 60

ttaagtaagg tcttggaccc taataaattc agggtatatg cattatgtat atgctctcat 120

ttagctgctc atctgatttc cattgggtga atcagttgtt ttgcagtacg tgggggtctg 180

tttatttttgt gagtttatgg tggagttcat tttgttgttg ttgtttttttc ttatctaggg 240

tttagggttt tgccctgtaa tcggtcttcc cctctctcct gcgcttgaat ttgacctgaa 300

acctcttgaa gtaggccctg gttttctggg ctttgacgaa aaccatggtt gtggatctcc 360

tctctcctgc tacggtcacc t 381

<210> SEQ ID NO 98
<211> LENGTH: 364
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 98

aggtgaccgt cctacttcac cgcagtgact tccatctggt tttaggaaac tatccctaaa 60

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tccttcacta gttgacgaat tgattgactc aaatcaactg tcggtcaaac ccactctctc 120

tgaaagtgaa ttctatgagt ctatacccaa cccaaatcaa taggttgagg taacagttga 180

cccgatttca ccttcaacaa atcatacctt tcccgaagag agtgaacatg attcaacaca 240

agttcttttt ggttcaccag attcaaatga gcttgggggt aatcctcctg ttccatcaag 300

acaagaagaa aatcctccca ctctcgtaac tcaagggtta atcctcccat ttctacggtc 360

acct 364

<210> SEQ ID NO 99
<211> LENGTH: 274
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (12)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (21)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (29)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (40)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (44)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (48)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (53)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (56)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (68)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (71)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (75)..(76)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (81)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (84)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (87)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (94)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (96)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (113)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (123)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (125)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (132)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base

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<222> LOCATION: (135)..(137)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (139)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (143)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (159)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (161)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (166)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (170)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (174)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (193)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (195)..(197)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (225)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (228)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (233)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (235)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (239)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (241)..(242)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (244)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (254)..(256)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (262)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (267)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (271)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 99

aggtgaccgt cncgggatag ntggagccna acaaagtacn gaanaaantg aancgcnctg 60

ggaagcgngc ngaaanntgg ncanacntgc cctncnactc ggttacccag ccnttctcta 120

ccnanaatta tnacnnnana gcnccatgct gggtttgtna naaaanaacn gctnttgata 180

aaattacata gantnnngaa cacgttaaga ggaatatggt tccanatnca ttntnaatna 240

nnanttaaaa actnnntatg tnctagngtc ncct 274

<210> SEQ ID NO 100
<211> LENGTH: 271
<212> TYPE: DNA

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<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 100

aggtgaccgt acagcacagg tatacaaatc atagaaatgg gcttctgtcc aactgtcagc 60

agaagcgata tgaaacccag aagcatcaac tctgctttca atttttcaag cgcttcatat 120

agagcctttt tatttcttct ggagagccaa ttgctagcat aatgaatacc atgttcaaga 180

agtaaagaga tgaccacaaa tgccaaacaa acaactgcta ctgcccaagt taggagtttg 240

ctctagagaa cggtcattgc cacggtcacc t 271

<210> SEQ ID NO 101
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 101

aggtgaccgt ggatatggga gcagagccgt ccgcagtgga tgctgcaatt caacttgaag 60

tggcagaagc tgtgaagact ctccaaatgg acaaggcacg aagacaaaac caagacaagg 120

atgagggcaa gagtggcaac gctgattcag atgacttgaa tgaaatggaa gtcaaagcta 180

aagcagccga acaactgctt gctgtgcatg gggcagcatt actacagaat gctctgaaag 240

aaaatttgtc gagtcatgaa atgcgggttg gttcaaatac aagggaggaa ggtgaagtta 300

gaaagaacag aaagggcatc aacgcagacc cctcactgat atcggcaaca ctacggtcac 360

ctaagccaat tctgcaaatt tccatcactg gcggggcccg ctccaacttc ctctaaaagg 420

ccaattcccc tatatgattc ttattacaat ccctggccct ccttttccac ttct 474

<210> SEQ ID NO 102
<211> LENGTH: 197
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 102

aggtgaccgt agcaggagag aggagatcca caaccatggt tttcgtcaaa gcccagaaaa 60

ccagggccta cttcaagagg tttcaggtca aattcaagcg caggagagag gggaagaccg 120

attacagggc aaggatccgc ctgattaacc aagataagaa caagtacaac acacccttgc 180

caaaaaaaaa aaaaaaa 197

<210> SEQ ID NO 103
<211> LENGTH: 208
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 103

aggtgaccgt atgagcaagg agggaacagt atgacaggca gtcaaagccc acgaggggtg 60

ccccactgcc tgcagcagcg cacttacttg gactaacaaa cttgtatcgt gattaaaacg 120

atgaacatcg tattgtggag tggagccact cgtgacctga ttctgtccta agtacttggt 180

cctggaatac aatattgcac ggtcacct 208

<210> SEQ ID NO 104
<211> LENGTH: 511
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 104

aggtgaccgt caaagtacaa tggagtcata tatccacttg aattgaaacc tctaatttaa 60

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aagttctcaa aaaatatttt atttacaaaa cagggaaaat aaaaaatgac tctatcaact 120

atacaatcct aacatccatc tcccgacaga cctccagtat atgtacaagg cgctgaaaga 180

aggctgatta ttttctattc cagctcgcat aacgtggttc ttctgaggct ttgcctattc 240

ctttctttaa aatctttcgc acgaaagatt ggcattgacc ttcggctaaa tctcagactc 300

cagggaacct tggactccct ttaaaaccta gagctacttt ttacgaaccc ctgcttctct 360

tgaacactta gggaacttat acttacaaaa cttcgggaac tccacccccct agctttgcag 420

gactccagca gattccccaa actgccagaa ggcatatttc catgcactgt taggggtgaa 480

ttcctactat caaaaccccc aaaacatcat a 511

<210> SEQ ID NO 105
<211> LENGTH: 430
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 105

aggtgaccgt atgggaacaa gtatgggaac aagaacgtta ttacataaaa gatggagatg 60

caacacagca taaattgatg ctaagtttgt tacaatgatg catacagctt aaccaagctt 120

ggaaatgaca tcattaagtg cggtcacagc ctctgcatag tatttctctg ccttgggtgt 180

atccttgctc cttgcagcgt agtccaggtt gtcaagggtt gtcaaaaagc ttggtggtga 240

aggttttgag gggcttcttc tggtccttgg gctttgagga gataacggtg tttgaagtcc 300

ttagcgaaag taagaaacct ttggaaccga agtccgttct tgacgttacc gcacgccttc 360

cttatctatc acttttcac ctccagaaat tgcttcccga atcccttgct ctcccacccc 420

ctgttccccc 430

<210> SEQ ID NO 106
<211> LENGTH: 362
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 106

aggtgaccgt agtgttgccg atatcagtga ggggtctgcg ttgatgccct ttctgttctt 60

ctacttcacc ctcctctctt gtatttgaac caacccgcat ttcatgactc gacaaatttt 120

ctttcagagc attctgtagt aatgctgccc catgcacagc aagcagttgt tcggctgctt 180

tagctttgac ttccatttca ttcaagtcat ctgaatcagc gttgccactc ttgccctcat 240

ccttgtcttg gttttgtctt ccgtgccttg tccatttgga gagtcttcac agcttctgcc 300

acttcaattt gaattgcagc atccacttgc ggaacggtct gctccccata tcacggcacc 360

tt 362

<210> SEQ ID NO 107
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 107

aggtgaccgt agtgttgccg atatcagtga ggggtctgcg ttgatgccct ttctgttctt 60

ctacttcacc ctcctctctt gtatttgaac caacccgcat ttcatgactc gacaaatttt 120

ctttcagagc attctgtagt aatgctgccc catgcacagc aagcagttgt tcggctgctt 180

tagctttgac ttccatttca ttcaagtcat ctgaatcagt gttgccactc ttgccctcat 240

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ccttgtcttg gttttgtctt cgtgccttgt ccatttggag agtcttcaca gcttctgcca 300

cttcaatttg aattgcagca tccactgcgg acggctctgc tcccatatcc acggtcacct 360

<210> SEQ ID NO 108
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 108

aggtgaccgt cgtgaaatag cgagaacggc gtggaacatc gcaacggcgg ggaggctggc 60

ggacgttgca cgtttctgga aggtatgcgg ctctctcctc cgcctcagtt tccatgaaga 120

ggtcctccct ggttgaatca tacgattgcg attgatcgag tacttgctgt atggctcggc 180

atcggcattg tggagacatt ctttcctatt cctcgcagca tctctccgat ggttgctctc 240

tccggagctc catgttatcc ccggcactga gacagtcgct gccgaatcgc aagagcttct 300

ttgtttttg caggcttctc caaacataat gcctccgggc ccctcaaccg aattctgcca 360

aatccacccc 370

<210> SEQ ID NO 109
<211> LENGTH: 578
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 109

aggtgaccgt ggacgacagt gagtgcagtc atcatgctct ccagtggact ttaagcaatc 60

tgcatcttta tggaagtgat gtatctcttg tggtttttca tgctcaacca ttggcagtct 120

tcaacagtgc tgcaacaatg ggcataacgt ctcccgaatt aattgaaact attgtgaatc 180

aacagatagg tttctggtca catctagcaa tacaaacaca aataactgtg gaacagagcc 240

acaaaactat gcttcagagc atctaattac acatatcttc tctaaaaccc ttgcataaaa 300

aataaactga atctcgacct tagcactatt gccaccatca tctcaagcaa acattctcta 360

gaataccatc ttcacaatgc actaaagtta cataagcact gaacttaaaa catttctgtg 420

acgaatgaag gaccaattca tcatactcag cctttgcatc caatctgttg aatgtgctga 480

aaaatgccca ataaacctcc atccaacact gtcttcctct ctgaggtgca cactgatttc 540

tgctgctgaa ccagtcggga ttccctgctc aacgtccc 578

<210> SEQ ID NO 110
<211> LENGTH: 297
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 110

aggtgcccgt ggaactactg ttaaatctgg aatcccttgt ctagctgtaa aaactcgaca 60

agtgcatgtt ggtattagta gggttaacag aagggttctt acccagattt acccctttgg 120

cggagatatt taaaaaaaaa gaattgtcat tatggtaaat aggtgtgaca ggttatcaat 180

agaataactg acgagagtaa actgataatt attaaggtta aagtgttcgt aaaggagact 240

tggactctag gttggatgcc tacacttaga gccgttcccg cacttggacg gtcacct 297

<210> SEQ ID NO 111
<211> LENGTH: 295
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 111

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aggtgaccgt ccagtgcggg aacggctcta agtgtaggca tccacctaga gtccaagtct 60

cctttacgaa cactttaacc ttaataatta tcagtttact ctcgtcagtt attctattga 120

taacctgtca cacctattta ccataatgac aattcttttt ttttaaatat ctccgccaaa 180

ggggtaaatc tgggtaagaa cccttctgtt aaccctacta ataccaacat gcacttgtcg 240

agtttttaca gctagacaag ggattccaga tttaacagta gttccacggt cacct 295

<210> SEQ ID NO 112
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 112

aggtgaccgt atgggaacaa gaacgttatt acataaaaga tggagatgca acacagcata 60

aattgatgct aagtttgtta caatgatgca tacagcttaa ccaagcttgg aaatgacatc 120

attaagtgcg gtcacagcct ctgcatagta tttctctgcc ttgggtgtat ccttgctcct 180

tgcagcgtag tccaagttgt caagggtgtc aaaaaacttg gtggtgaagg ttttgaaggg 240

cttcttctgg tccttgggct ttgaagaaat aacggtgttg aagtccttac caaaggttaa 300

taaacctttg gagccgaagt cgttctggac gtacggccac cccttcctta tctatcagct 360

ttttcacctc caagaatttg cttccccgaa ttcctttgct ctcccagccg cctggtcccc 420

cgaaaagggc tgaatataaa accgtcctca acggcattcc attcctccct cgtctgaaac 480

acttccccgc tgcccccgag gtgaagggcc atcaacttga tgaacggctt ttgcaaggct 540

ctgaccccgg ccccgtcact aaccaattct gcaatc 576

<210> SEQ ID NO 113
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 113

aggtgaccgt ggggaacaac tacatgacaa atcatttctt tgtggtggat gtactggaca 60

ccaaataagt gttgagagtc cactggctct gtacgcgtgg cagaatcaca acggacttga 120

gaaagttgaa gatggaattt gtatcgctag atggccagac catgttgctt caagggatgc 180

actcgtaacc cccacagtct gtctctaccc actagatgga ggctgacatg agacatggag 240

acattaattg ggttgtggag ttaaagatct ctcacgttcg gggaaaatcc aagccatcat 300

acttatatat ccgtcccgtg catgtaacct cctccactct gtcccttagg cccgttgttg 360

cct 363

<210> SEQ ID NO 114
<211> LENGTH: 583
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (24)..(25)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (54)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (71)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (75)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

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<221> NAME/KEY: modified_base
<222> LOCATION: (77)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (85)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (111)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (119)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (124)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (153)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (177)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (187)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (194)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (213)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (242)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (258)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (270)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (279)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (281)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (299)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (312)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (316)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (322)..(323)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (361)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (409)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (414)..(415)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (457)..(458)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (468)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (480)..(481)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (487)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base

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<222> LOCATION: (489)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (493)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (511)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (515)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (558)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (565)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (575)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 114

aggtgaccgt atgagcaagg aaannaccgc actggctccc agcagcatga acanccaggt 60

cccaaccata naccncntgg agaangtgat caagatatta gcgacagtgt nattgtacnt 120

ctcnccaaac acattataca cgataagaga gcntaaacta ctctattcct ttgacgnagt 180

gactacntga gtanaagcga tcattatctt gcnaactttg catgaaaaac aacaaaccca 240

cntccagttt ctctatantc tggccccacn atgaataana ntcctgccat aataatgant 300

ctttgtcccc anaganaaat tnnataagac aggagcccac tgttgcttgc atgactacca 360

ntcactttaa ggcgttgcga atcccggtcc taaccatctc cataccatng gcanncttta 420

ctttccaact gcccaagact gtgaacaggg cggttcnnac cctataantt ttagcctctn 480

ntcgaancnc ttnttttcgt tccccggaaa nccgnttccc acccctttgga accttttttt 540

tttgccgggc cccaggcnaa ttctncaatt ccccnctggg ggg 583

<210> SEQ ID NO 115
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 115

aggtgaccgt ggcggaggtt agggaagttt gacttctcat tttctcacgc actcctctcc 60

ctcgtaacct cggtcgagtc gatggcggct ttttagtcga gtgtgctaac gcaccctccg 120

ggcctcaaaa tttccagcta ctcgtatttg atcaatgctg aaatcgcgta atcacgtaga 180

taataaagcg taatgaattc tataatgaag catgtttctc tatagttcat gttgccgaga 240

aggaataatg aaaatgaagc cttatatatt atctggggct caaggagatg ttatcttttc 300

tcttccttgg ttagagaccg tcaccttcac tttgaattgg ataaagcttc atttgtttaa 360

gacctcccac ccgtaaatac atacggtagc cttcttatgt tagaaacata cgtcacctac 420

gcagaattgt tagaatgaaa tga 443

<210> SEQ ID NO 116
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 116

aggtgaccgt ggaacaagat gattagttct catgcgggcc aggatgatta gttctcctat 60

ggcaactgtt ggacaggatg attcgttctc ctgtggacag gatgattagt tctcctatcg 120

-continued

aggcatccta cccaagcagt ttgggactca tgggaagtac ctctcatctg atcaatgagt 180

aggaaatggg gttagggacc attaagtagt attatcgatg gatgcattgt tgtatctatt 240

gtactcccta tgctagaatg aactccattg atctgggatc aatgaatact gtttctggga 300

atcattgaaa atttgtatga acacactctg aacactgaat ttccggttca ttggaagaga 360

tggttttaaa cactctcctc atctcatttc ttccccttcc ttattccaac caaatttggg 420

ccaccctgcc aggaaattca tttgatggtt ggaaaatacc acgggcccta accaattctg 480

caa 483

<210> SEQ ID NO 117
<211> LENGTH: 593
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (11)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (24)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (27)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (39)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (48)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (50)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (54)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (56)..(57)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (59)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (63)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (66)..(67)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (71)..(74)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (78)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (92)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (96)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (112)..(113)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (126)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (146)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (167)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (173)

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<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (184)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (186)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (197)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (203)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (206)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (252)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (254)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (258)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (268)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (276)..(277)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (291)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (300)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (304)..(305)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (324)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (331)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (339)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (344)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (348)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (353)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (373)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (380)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (401)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (416)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (430)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (433)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (444)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

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<221> NAME/KEY: modified_base
<222> LOCATION: (472)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (475)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (481)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (484)..(485)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (497)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (502)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (506)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (508)..(510)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (520)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (529)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (533)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (561)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (568)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (579)..(580)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 117

aggtgaccgt ncatctctac catnatncct ccctcccgnc tgtatcancn ggcntnnang 60

tcnttnncta nnnnaagntt aatcctatcc cnttanagtt gacggtctct anncctagaa 120

gagaanccat aacatctcct tgagcnacac atgggatata ccgccanctt atntaatact 180

ttcncngcac ggtaacngac canaancatt cttcactata gaattcatgt cgcttcatta 240

tctacctcat tncnccanat ccccttnat ctcatnnatt tatctagaaa nttctgaagn 300

tccnnaaggg ttcgttttgc accncccaa ntaaaaaanc cctnccgntt acntcgaacg 360

aaggttttca aangaacagn aattccttta caaaaatcaa naattttaac ttcccnaatc 420

cggccccccn gtncccgaaa cccnatttct acgattgcat caccccgggg gnccnctcaa 480

nccnncttct taaaggncca tncccntnnn tgatcctctn ccatccaang gcnccttcc 540

acttttattg gaaaaccccc nttcccntt ttacccttnn aaggcccctt ccc 593

<210> SEQ ID NO 118
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (237)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 118

aggtgaccgt ggaactactg ttaaatctgg aatcccttgt ctagctgtaa aaactcgaca 60

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agtgcatgtt ggtattagta gggttaacag aagggttctt acccagattt acccctttgg 120

cggagatatt taaaaaaaaa gaattgtcat tatggtaaat aggtgtgaca ggttatcaat 180

agaataactg acgagagtaa actgataatt attaaggtta aagtgttcgt aaagganact 240

tggactctag gttggatgcc tacacttaga gcccgttccc gcacttggac ggtcacct 298

<210> SEQ ID NO 119
<211> LENGTH: 631
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (591)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (607)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (609)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (616)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 119

aggtgaccgt gggggatggg gccgtgggga agacttgtat gctcatctcc tacacaagca 60

acacgtttcc aacggattac gtgccgactg tttttgacaa ttttagtgca aatgtggttg 120

ttgatggcaa tacagtaaac cttggcttgt gggacactgc agggcaagaa gattacaaca 180

gactgaggcc attgagttat agaggtgcag atgcttttct gcttgccttt tctctgatca 240

gcaaggctag ttatgaaaat atatcaaaga agtggattcc agaacttaga cattatgcac 300

caaatgtgcc aatcattctt gtgggaacta aattagattt gcgtgatgac aagcagttct 360

ttgctgatca tcctggagca gcccctataa caacagctca aggtgaagag ttgaagaagc 420

agattggagc agcagcatat attgagtgca gttccaaaac ccagcagaat gtcaaggctg 480

tttttgatgc tgcaattaaa gtggttcttc agccaccaaa gcagaaaaag cggagaaaaa 540

agcagaaaaa ttgttctatt ctctaagaaa aatgtggatg ttctgaacgc ncttcactga 600

caataangnt gacgtnggaa tatcttcctc c 631

<210> SEQ ID NO 120
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 120

aggtgaccgt aagcacaagt cgtcaaaatt atctctattc cggcagtaaa aacctatagc 60

taatgatgga tcaataccac taagtggcag ctggcgtaca tctctgcaat gataagaacc 120

agtatcagtc cccatataat caggagatat ctccagcacc tgctgcacta catgtggatc 180

ttagtacaga gcctgatcat cctgaacacc aacaatatac gttgaagctc cgggctttcc 240

accagcaata ccaagacttt ggggaaatgt gaacgtttca cgaagtgatg gtacatacct 300

tgggttgatc ttctctacac caagaacaag cggcaccaaa atcaggatag gcacttggtc 360

ttccccttct ccattggacc actctgaaca caagcctcgc agcatcatca atgcagataa 420

ctgggcgccc tccacggtca ctt 443

<210> SEQ ID NO 121
<211> LENGTH: 327
<212> TYPE: DNA

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<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 121

aggtgaccgt gccatagcgc atggcgtgta actggatgag accgcatggc tcaaatctgc 60

taggaatcaa catgaaatca gctccagctg ttatcatatg agcaagtggc acgttaaact 120

ttgctactcc cctgacgttg tctggatatt tctcttcaag ctcttcaagc tgcttctcca 180

agtacttttt accggtgcct aggataatta actgcacgtt ttcatctgca attagaggga 240

cagcttcagc aagaatatct ggacctttct gctcttcaag tcttccaata aatcctataa 300

caggaatatc tggatccacg gtcacct 327

<210> SEQ ID NO 122
<211> LENGTH: 284
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 122

atgtgaccgt caaaagggca tataaatcgg ggagctcaat ggcaagaatg tacgatttct 60

ggcctcaagt cgccctgaat ttggtcaaca acatcttgat agagcgagag gacgctccca 120

attaagatct ggaaactgtc gagagtgatt gaggtcattt ttaatctaaa ctgaattgtg 180

gggacaattt ttcaattcag atccttctag caaagcaaag caaagcttaa cagtattgta 240

tccatgagaa tggattctgc acaggtcagg ctccacggtc acct 284

<210> SEQ ID NO 123
<211> LENGTH: 412
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 123

aggtgaccgt ggagaagaga acgctttgcc gactctctgg gatgcccttc cctccatagc 60

cgtcgtggga ggacagagct ccgggaaatc ctctgtgctg gagagcatcg ttggaaggga 120

ttttttaccg cgtggatcag gtattgttac tagacggccg cttgtccttc aacttcacaa 180

gactgatgaa ggcagcaggg attacgccga attccttcac caacccagaa agaaatacac 240

cgactttgca ctggtaagga aggaaattgc ggatgagact gatcgaatta cagggcgttc 300

caagcaagtc tcaagtgtcc caattcacct tagtatttat tcacccaatg tttgtaaatt 360

tgactctaat tgatctccct gggttgacaa aagtggctat tgacggtcac ct 412

<210> SEQ ID NO 124
<211> LENGTH: 235
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 124

aggtgaccgt gcaatattgt attccaggac caagtactta ggacagaatc aggttacgag 60

tggctccact ccacaatacg atgttcatcg ttttgatcac aatacaggtt tgttagtcca 120

agtaggtgcg ctgctgcaga cagtggggca gccctcgtgg gcttggactg cctgtcatac 180

tgttctctcc ttgcttcagg ctctactgct gttgctgctg ctgatacggt cacct 235

<210> SEQ ID NO 125
<211> LENGTH: 353
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 125

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aggtgaccgt acatacaagg tcttatcacc agcagcaaga ataatcagtt ggccatcttc 60

tgcaggcttc ttgctgcctg agacaggagc ctcaagaaat cttccccct tttcaatgat 120

tgcctcattg atctttgttg aagtgatagt atcaactgtt gacatgtcaa tgtatccttt 180

tcctgtacac atttgctcta ggacaccatc cgagagggca gcaggaggat cagacaggat 240

ggctatggta tagttgcact tctttacaac ttcggcagga gtgcttccta tggaagcacc 300

ttgctgaaca agttcttcac acctagacat tgtcctattc cacacggtca cct 353

<210> SEQ ID NO 126
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 126

ggtgaccgta catacaaggt cttatcacca gcagcaagaa taatcagttg gccatcttct 60

gcaggcttct ggctgcctga gacaggagcc tcatgaaatc ttccccccctt ttcaatgatt 120

gcctcattga tctttgttga aatgataata tcaactgttg acatgtcaat gtatcctttg 180

tcctgtacac atttgctcta ggacaccatc cgagagggca gcaggaggat cagacaggat 240

ggctatggta tagtcgcact tctttacaac ttcggcagga gtgcttccta tggaagcacc 300

ttgctgaaca aagttcttca cacctagaca tttgtcctat tccgcacggt cacct 355

<210> SEQ ID NO 127
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 127

aggtgaccgt ggaggggctc cagttatctg cattgatgat gctgcgaggc tgtgttcaga 60

gtggtccaat ggagaagggg aagaccaagt gcctatcctg attttggtgc cgcttgttct 120

tggtgtagag aagatcaacc caaggtatgt accatcactt cgtgaaacgt tcacatttcc 180

ccaaagtctt ggtattgctg gtggaaagcc tggagcttca acgtatattg ttggtgttca 240

ggatgatcag gctctgtact tagatccaca tgtagtgcag caggtggtgg agatatctcc 300

tgataatatg ggggttgata ctggttctta tcattgcagt gatgttcgcc actgccactt 360

aatgctattg atccatcatt agctataggt ttttactgcc cggaatagaa ataattttga 420

caacttgtgc ttacggcacc t 441

<210> SEQ ID NO 128
<211> LENGTH: 437
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 128

aggtgaccgt ggaggggctc cagttatctg cattgatgat gctgcgaggc tgtgttcaga 60

gtggtccaat ggagaagggg aagaccaagt gcctatcctg attttggtgc cgcttgttct 120

tggtgtagag aagatcaacc caaggtatgt accatcactt cgtgaaacgt tcacatttcc 180

ccaaagtctt ggtattgctg gtggaaagcc tggagcttca acgtatattg ttggtgttca 240

ggatgatcag gctctgtact tagatccaca tgtagtgcag caggtggtgg agatatctcc 300

tgataatatg ggggttgata ctggttctta tcattgcagt gatgtaccca ctgccactta 360

gtgctattga tccatcatta gctataggtt ttactgccgg aatagaaaaa ttttgacaac 420

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ttgtgcttac ggtccct 437

<210> SEQ ID NO 129
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 129

aggtgaccgt gctaggacac acaatttctc agcaaggatt acaggtggat cctaacaaaa 60

ttgctataat tcaaaaggtt ccacctcctt aaaaggtaag agatgtttgg agttttctag 120

gcttggcagg atattataga agattcatca aagatttcat taagctagcc tcgccattgt 180

ctagcctctt agggaaagat gttgagtttc aatggactga tgactgccaa ggggctctgg 240

atgagttgag agataagctg gtatccgccc cgatcttgag aggtctaaac tgggccctac 300

ctttccacat ccacattgat gcctcgaaca aagccatagg ggcagcctta ggacaagttg 360

aagagaaaat accatatgcc atatactttg tcagcaaaaa tctgtctaag gcagaactga 420

actatacggt cact 434

<210> SEQ ID NO 130
<211> LENGTH: 427
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 130

aggtgaccgt catattcccc tctatagcag cactaacaat ccattttctg agtgcatcag 60

aaaatcaaca cacggtaaat gtcttgagac taacgagaaa ttaataatca cgttgtacaa 120

agaacagtat gtcccgtcac gtcacgagtg ccctgagaga tcatccaact ttctctgaac 180

cctcgtgtta cacgcacgca aaatcaagga tcagttgtag ttattgctgg cgtgacagac 240

gtgacaccta ctgttccgct acaaacgata taattgaatc catgatcgga ttatgtatta 300

tgatcttagc gcagtggtta tgaaattatg atgaatttgc ttatgatttt ctcagcgttt 360

gtggaagaat ctcgctattg aaaacttccc cgtatatttc caaacttatt atcatcccac 420

ggtccct 427

<210> SEQ ID NO 131
<211> LENGTH: 261
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 131

aggtgaccgt acagcattta ttgatgttct attttgttgt ttgcaagttt ttccgattcg 60

ctgtgaggca cggaaaacga gataagttgt aaaagtttgc tcgctgattt gaggcacgga 120

aaacgagata agttgtaaaa ttttgctcgc tgatttttg ctgaatattt ctctcactat 180

aaaaagcatt ttccagaaat aagaaggagc tttcgaactg gttttcccca agagttgtag 240

ggggtttttc cacggtcacc t 261

<210> SEQ ID NO 132
<211> LENGTH: 262
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 132

aggtgaccgt atttatggtc gcaggcacaa attctgctac tgtagaaggg ttcttaccaa 60

ctttaggtag aaggcgagga gggctttatt agtacagttc tgtgtaatct taatgatatt 120

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ttttgcacta ttattttatg gtaaaaggat tgatttgtct tttgcaaagg ccttaggatt 180

gtttatttac ctttgggcta agggaggagg taaatttttc acattgggaa aaaaaatgcc 240

tcggtcgttg tcacggtcac ct 262

<210> SEQ ID NO 133
<211> LENGTH: 126
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 133

aggtgaccgt gccagtatga cagatggaac catgcagcta gccaccaaat tgtaaacatc 60

aaattttgtc ttcaatataa gttgcaaatt cttaattaat tatgatcacc atttcaacgg 120

tcacct 126

<210> SEQ ID NO 134
<211> LENGTH: 238
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 134

aggtgaccgt gaatagaagc gaacacatcc ttgttgctga atctaacgac caatcggtat 60

ttgggtgtgt tgtacttgtt cttatcttgg ttaatcaggc ggatccttgc cctgtaatcg 120

gtcttcccct ctctcctgcg cttgaatttg acctgaaacc tcttgaagta ggccctggtt 180

ttctgggctt tgacgaaaac catggttgtg gatctcctct ctcctgctac ggtcacct 238

<210> SEQ ID NO 135
<211> LENGTH: 245
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 135

aggtgaccgt ggtagaggag gcaggcactc atctaacagt cgaaagccct ttacaaaggg 60

gaatggtacc agcatagaga agaaacacag acggtttgaa gaggatgatg gatctgccat 120

agatgaacga tcaaataagg ttcaaaagct ggaaaatgat ggtgaattcc atgcatccca 180

cttggctctg tccctcaagt tgaatatacc tggacgagag gtattgcatt tcccaacggt 240

cacct 245

<210> SEQ ID NO 136
<211> LENGTH: 239
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 136

aggtgaccgt actgataata gaagaggcag ggaaagagaa atcaatgata atagaagagg 60

cagggaaagg gagatcaatg gcatcatgct acttcttgta gctgtttaac cttagtgatg 120

taatcttcca tggcagactc gggggtttta tctttaagtt gaatttccat gcatcccctt 180

gggctctgtc ctccagttga atatcctgga acaagaggtt ttgctttcca cggtcccct 239

<210> SEQ ID NO 137
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 137

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aggtgaccgt gagaaggcaa ctttatcccc tgctaaacca agtccagaaa tgaggaaaat 60

atgtgaaaac tgaattgcta tatatgatgc ctagtcttgg cctctcaatt acaagttcaa 120

cgtcttcaaa tgattgaaat atggaccttc ttaaccgttc tggaaatcta tcaatcttca 180

aaattttgaa actttgcctc gatcttggag tgatcagact tgatttctaa tcctagaaat 240

accctatcac tggctacctg gtctgtacgg tcacct 276

<210> SEQ ID NO 138
<211> LENGTH: 274
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 138

ggtgaccgtg ggataggcag aagcaagaaa cacagaagtt cttccgggaa tgtaagcgct 60

gacagtgggg gagaaagtag tgaacaagga catggtcggt atgaaataca tggcaggcga 120

tggatttcaa gggattaagc atctcaatgg atatttacta ttggactgta gtaactttcg 180

ccatcgcttt ttgaacacat ctgtggctta actgtcatct gtaatggtaa gcgaaccagg 240

ttttgttctg aaccacttgt atgtacggtc acct 274

<210> SEQ ID NO 139
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 139

aggtgaccgt ggtggagcga ttagtgattg tgataaaggg agcatcaata tctatgtaga 60

cgccgtataa aggtggaaaa ggtatgtttt gcaggtattt ctttgtaaat ggtttataat 120

gggttaagct cggatatatg aggtttatat ataagtcctg ttagtgtcag tcttaccagc 180

cttcctccag tgatcaaatg tgctctaaca aagtgatttt gaagtgtcaa ggtcaaatta 240

tgtcatttca gtgagtcttc aaacaaaatt tggtcactag gcattaggtc taagggtttg 300

cttgaactcc ctctagagtt gtccaaatgg gcgggctatg tcatcattta agctgaatct 360

atcatccaat caataaggtt tttcattatc atgtcagtgt ctaaatgagt cattttaccg 420

tcttgttcac ggcttcactt gtgcctttgg caaattcaat tccctcctcc aagggtttga 480

aaccaattct cttggacggc ccctaaacca aatctgcaaa atccac 526

<210> SEQ ID NO 140
<211> LENGTH: 538
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 140

aggtgaccgt ggtggagcga ttagtgattg tgataaaggg agcatcaata tctatgtaga 60

cgccgtataa aggtggaaaa ggtatgtttt gcaggtattt ctttgtaaat ggtttataat 120

gggttaagct cggatatatg aggtttatat ataagtcctg ttagtgtcag tctttccagc 180

cttcctccag tgatcaaatg tgctcttaca aagtgatttt gaagtgtcaa ggtcaaattt 240

tgtcatttca gtgagtcttc aagcaaaatt tggtcactag gcattaggtc taaggtttgc 300

tttaactcct tctaaaagtt gtccaaatgg cgggctatgt catcatttag ctgagtctat 360

catcatcata ggttttcatt atcatgtcag tgtctaatga gtcatttacg tcttgttcag 420

ctcagtgtgc ctggcaattc attcctctct aaggtttgaa ccattctctt gacggcacta 480

agccaatcca cactggggcc gtctattgaa tcaacccgga cactgggtta caggcaac 538

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<210> SEQ ID NO 141
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 141

aggtgaccgt ccaagaagaa attggcttca aaaccctagg agagggaaat gaacttgcca 60

aggcacaact gaagcatgaa caagacgtaa aatgactcat tagacactga catgataatg 120

aaaaacctat gaatgatgat agactcagct aaatgatgac atagcccgcc atttggacaa 180

attttagaag gagttaaagc aaaccttaga cttaatgctt agtgaccaaa ttttgtttga 240

agactcactg aaatgacaaa atttgacctt gacacttcaa aatcactttg taagagcaca 300

tttgatcact ggaggaaggc tggaaagact gacactaaca ggacttatat ataaacctca 360

tatatccgag cttaacccat tataaaccat ttacaaagaa atacctgcaa aacatacctt 420

ttccaccttt atacggcgtc tacatagata ttgatgctcc ctttatcaca atcactaatc 480

gctccaccac ggtcacct 498

<210> SEQ ID NO 142
<211> LENGTH: 350
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 142

aggtgaccgt gatagacccc aagaaaaata gatccaaccc tcagagggac aaagacttat 60

aaagactaga agagtgaatc aacctattct atttagaata tatatttttg gggtgcttgc 120

ttatcgtttt gggggttaat gtatgtcgta ctacggtctt atgccctaat ttgcccattg 180

aaatcaacta aattgacagt aaccgactaa aagttggtcc acactaagat atcgatgacc 240

aacgatcata aaggtgtcca tgatcctaat agtatatgtg tcaattaatg taactttggt 300

gctacaacat aaaaccattc gtggggatcc tccttttttat gcggtcacct 350

<210> SEQ ID NO 143
<211> LENGTH: 346
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 143

aggtgaccgt gggaccgacc ttgactacag gccaaaattt tgactgttga ccagcgttca 60

cttctgtatt tttggttggt atgagcaaca ttgacttgct ggaaattgac caggtttgac 120

tggtatttgg acttggattt tggcacagat ttctagacaa tttgtatttg taaaccttac 180

agaagaataa tttatcgaag aagaaaaatg ctaggtttcc cctcaagttt gggtttccca 240

agggaaaaat tgttgtccca atggttgaat tttccaaagg tctcctaacc cgacaatacc 300

tcctaagaat tccttaattt aacctttctt gttttcacgg tcacct 346

<210> SEQ ID NO 144
<211> LENGTH: 335
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 144

aggtgaccgt gaaggagcag caacaatttg attttgtttg ggtagatcgg ggattttctc 60

gtggaacata cctgattgag tataaactaa gtcaaggtac tgtgcttgag aaattacttg 120

-continued

ctcctcagta actactctgg ccttagctac atcctcagtg atcttgggta gtaaagattt 180

tacaaaccat tcagctaaga tctgatccgg gatataaact ttcactaaac gtcgtcgacg 240

tctccattca tggatatgat ctgaaatgta agtggacgtt gactgcttta acgaagttaa 300

taattctgtg ccattttcat atctgacggt cacct 335

<210> SEQ ID NO 145
<211> LENGTH: 344
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 145

aggtgaccgt acctaatggg aagacacttc aaggtaaaaa caaatcatga tagtcttaaa 60

taccttttag aacaaagatt atattcagaa caacttgctg gaagtgtacc aagtatgact 120

ggtattgaga cttagatctt cgcacagatt tcaagacaat ttgttgttgt aagactcact 180

cacgaaaagt gatgtggata tgaagaactt ccctgtcgcc tcttggttag gagtctccca 240

ctcataggaa ttgtgtaact tataacttgg tccactaaag aagttaggta cagtgtgttc 300

ctttaccagg ttccctgttg taacttacaa atctacggct acct 344

<210> SEQ ID NO 146
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 146

aggtgaccgt cactggaggt ttgagatgct tgatcggtac tgaaatgaga catgatcaga 60

ataggacctt gttgaggccg tgtctcaccc cccatccaca atcttttgta attttgagtt 120

tcgtttagaa catacttgta ggataaaact taccttactc atggatcatg gctgtatatg 180

tttatcgacc agagacagat atgccgaatg aaagcgagtc tagtattcta atgcaatata 240

ttggtagtat gggacatagt actgaacact tgtatagtac ggtcacct 288

<210> SEQ ID NO 147
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 147

aggtgaccgt ggtctcagtt atgccatatg tccgcccctc catatgatgc tccgcctcta 60

tgggggtctt tgcgatgttg atatctagta gtacttcttg tcctattgca gcaacctgta 120

ctggtgttgg tgttggttat gggtctccta cgcgatggag atatgagaca cccataggtc 180

gaacaggtct aatatctgga atccaacgct atttgttgta gaagaaacgt tgctcccgtc 240

ctttagcttt ggctggtcac tatccttacg ctccacgtac ggtcacct 288

<210> SEQ ID NO 148
<211> LENGTH: 208
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 148

aggtgaccgt tgggaaatgc aatacctctc gtccaggtat attcaacttg agggacagag 60

ccaagtggga tgcatggaat tcacttaaag ataaaacccc cgagtctgcc atggaagatt 120

acatcactaa ggttaaacag ctacaagaag tagcatgatg ccattgatct ccctttccct 180

gcctcttcta ttatcagtac ggtcacct 208

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<210> SEQ ID NO 149
<211> LENGTH: 197
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 149

aggtgaccgt caaggcaaag tgtcatgcca ctcattggaa ttagttaata tagctaattt 60

gagatattac agtcaactgt gggtatatgt atgtgagatc aaggtgcagt ttagatatta 120

tcagtggtgc agtttagata ttatcagtgt ttgtgaatct gcatactgct tttggttggt 180

tctaactacg gtcacct 197

<210> SEQ ID NO 150
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 150

aggtgaccgt agacatatat catggaaaac ccaagtaaca tacaaacaca aaacacatgg 60

aaacttcata aaacctccac tcgtcataag ctttattgct atgttattgt ggtgttgcat 120

cgtacttagt ggaggttatt gttatgttat gtgttctatt ttcctcccga acgcccttcg 180

gaattgagct aaccgtggtt aacaacatgt gggctttttt tctcgacagt atatatataa 240

taaatcttta ttttttaaa aactaatgct attgcattta tatactggaa aaaatgattt 300

ttcttgtatt atcgaaaata ataatttagt ttcttgataa tcacttggaa ttaagaaatt 360

acaaacccta acaacatcaa gaaattttaa aacacataag ctagaaattt taaaacacat 420

aagcgtgaca acaagaagat caaatctaat acttgcttgg gccggagatt atggattcat 480

gaagcgattt gacagcgtcc attgatcttc ctctcccacg gtcacct 527

<210> SEQ ID NO 151
<211> LENGTH: 171
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 151

gggggtaggg gtgtttatac tgagcatact tcgaaagtgg ttcaccacca ccatgatgac 60

taattgttcc tgactttggt agacctataa taaattccat agaaacctcc gtccatattg 120

atgccggaat gggcaacggt tgtaatgtgc ctggtacttt gacggtcacc t 171

<210> SEQ ID NO 152
<211> LENGTH: 412
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 152

aggtgaccgt tgggaaatgc aatacctctc gtccaggtat attcaacttg agggacagag 60

ccaagtggga tgcatggaat tcacttaaag ataaaacccc cgagtctgcc atggaagatt 120

acatcactaa ggttaaacag ctacaagaag tagcatgatg cctagacaaa tagctttgct 180

caacacatcc tgatagtgta cactaaatcg cacaacttta ctactacaaa gaaagatcgt 240

tgacaccttg acaaatagct ttgctcaaca catcccaaca atttggattg cgaataccga 300

ctccaatttg tacttgatcc atatgtcgtt gcgatgtact agttcctcta tacatatgtt 360

tctgcaagaa tcggagttgg acctcttctt ccctgttatc agcacggtca ct 412

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<210> SEQ ID NO 153
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (307)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 153

aggtgaccgt ggataagaga acgctttgcc gactctctgg gatgcccttc cctccatagc 60

cgtcgtggga ggacagagct ccgggaaatc ctctgtgctg gagagcatcg ttggaaggga 120

ttttttaccg cgtggatcag gtattgttac tagacggccg cttgtccttc aacttcacaa 180

gactgatgaa ggcagcaggg attacgccga attccttcac caacccagaa agacatacac 240

cgactttgca ctggtaagga acgaaattgc ggatgagact gatcgaatta catggcgtgc 300

caagcanagt ctcaagtgtc ccaattcacc ttaatattta ttcacccaat gttgttaatt 360

tgactctaat tgatctcctg ggttgacaaa attgctattg acggtcact 409

<210> SEQ ID NO 154
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 154

aggtgaccgt tgggaaatgc aatacctctc gtccaggtat attcaacttg agggacagag 60

ccaagtggga tgcatggaat tcacttaaag ataaaacccc cgagtctgcc atggaagatt 120

acatcactaa ggttaaacag ctacaagaag tagcatgatg ccattgatct ccctttccct 180

gcctcttcta ttatcattga tctctctttc cctgcctctt ctattatcag tacggtcacc 240

t 241

<210> SEQ ID NO 155
<211> LENGTH: 289
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 155

aggtgaccgt acatacaagt gctcagtaca atgtcatata ctaccaatac atttgattag 60

aatacgagac tcgctttcat tcggcatatc tgtctctgga tgataaacat ataaagcctt 120

gatccatgag taaggtaagt ttgaagctac aagtattttc taaacgaagt tcaaaattac 180

ataagattgt ggctggggcg tgagaaacgg cctcaacaat gtcctgttct gatcatgtat 240

catttcagta ccgatcatgc ctatcatacc cgcctggtga cggtcacct 289

<210> SEQ ID NO 156
<211> LENGTH: 209
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 156

aggtgaccgt actgataata gaagaggcag ggaaagggag atcaatggca tcatgctact 60

tcttgtagct gtttaacctt agtgatgtaa tcttccatgg cagactcggg ggttttatct 120

ttaagtgaat tgccatgcat cccacttggc tctgtccctc aagttgaata tacctggacg 180

agaggtattg catttcccaa cggtcacct 209

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<210> SEQ ID NO 157
<211> LENGTH: 191
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 157

aggtgaccgt atagtgtcaa gcttttctgg attggataat ggacggcggc ttgcgacata 60

catctacaca ttctgtaaca agtacactct actgcaacag cagacccaat ttcacctctt 120

cagtcagcca gagatctcga tggatttggg ttgaggaggt tggggttctg cctgcttcgg 180

cacggtcacc t 191

<210> SEQ ID NO 158
<211> LENGTH: 415
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 158

aggtgaccgt gctaagtaat tatcatctgt acctgtgctt gctgcaggaa gtaaaccaac 60

ccgactagtc tttttaataa tacagggagc cttgccacca atttcctctt gaagcaccca 120

tattggacgg gtttgtgtca tcctctgtat tatccttttt catcccaagc aggctgtctg 180

tttttgtagt agaaggatca caacacagat caggccctcc atagtacaaa gaagaaccga 240

ggaaagtatc attaacgttc tgactcctgc catgaaggct tccactatga ccttgaccct 300

tttgtgaatt actgccattt agaccttgac tggctcttgc aaccaaatgc cccagaatgg 360

aacttctttg tgctccagtt ccattgtggt tagttgaatc cctaccacgg tcact 415

<210> SEQ ID NO 159
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 159

aggtgaccgt gcaatattgt attccaggac caagtactta ggacagaatc aggtcacgag 60

tggctccact ccacaatacg atgttcatcg ttttaatcac aatacaagtt tgttagtcca 120

agtaagtgcg ctgctgcaga cagtggggca ccccccgtgg gctttgactg cctgtcatac 180

tgttccctcc ttgctcctgc tcttgctctc gctgggctgt ggtgagttac taacctggtt 240

cgacccacaa gggcttctca ctagggcgtt aggctgcatg gatctgccag atattgtggt 300

tgcaagggac agaggcatga gacacaggcc tttgctttgc agaaactgca ttgctgaccc 360

catgttttca tccatcagtt ttgctacctc tccttctgtt atggacggtc acct 414

<210> SEQ ID NO 160
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 160

aggtgaccgt atccgcagca gcaacagcag tagagcctga agcaggggac ctaattacag 60

tcaaaagtcc agggctacca atgcctgcta acagcgcact tacttggact aacaaacttg 120

tattgtgatt aagacgatga acatcgtatt gtggagtgga agccactcgt gacctgattc 180

tgtcataagt acttggtcct ggaatacaat attgcacggt cacct 225

<210> SEQ ID NO 161
<211> LENGTH: 234
<212> TYPE: DNA

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<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 161

aggtgaccgt atccgcagca gcaacagcag tagagcctga agcaggggac ctaattacag 60

tcaaaagtcc agggctacca atgcctgcta acagcgcact tacttggaac taacaaaatt 120

tttattgtta attaaaaacg aataacatcg tttttgtggg agtggaacca ctcgtgaact 180

gaatcctgtc ctaagttctg ggtcctggga ataacatatt gcacgggtca cctt 234

<210> SEQ ID NO 162
<211> LENGTH: 548
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 162

aggtgaccgt tacagctagg gaagacttta aaagtttgta aaactaagca tagctcttaa 60

acactgaagt taaaagacat gattggaatg tgcaagtggt tcagtatcca aatattgaag 120

gttgcagaat atggagctac tgtgcaaacg agtaacttta tctatatttt cacaagatca 180

tacaatggga aacgttgaga taacaactgc atcggtgaac cagaatagtt ataaaagttc 240

ttgcaagtaa agggatgaat aattgcatgg ttggaattaa gaatgaccat gtagagctgc 300

tatacagatt ctccaaggtt ttatatttga ggagtgcgcg ctattgatgt tgtgcaaaaa 360

tttcagaaat taagttctgc ggcatttatc aaggttgttt gagccattta aatagcaagt 420

ttttgtttct ccaagtactt tcaggaaagc agatagctct agttataatg ctccagtgac 480

aaacacatct agttggggca gtgaatgacg cttttgtcat tctcttttgg tttcaggcac 540

ggtcacct 548

<210> SEQ ID NO 163
<211> LENGTH: 176
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 163

aggtgaccgt ggacaaactc tagaacaggc atagctttca tgttcagttg tttttaaaga 60

gcagtcctcg cagcagatcg tgcagcttcc tgcttcactt ccgttgattt tcctgatctg 120

aaatacccgt aaacttgctg aagaacccaa atacttaata gcgtctctaa acaaaa 176

<210> SEQ ID NO 164
<211> LENGTH: 699
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 164

aggtgaccgt gcctgaaacc aaaagagaat gacaaaagcg tcattcactg ccccaactaa 60

tgtgtttgtc actggagcat tataactaga gctatctaca agccaaaaca gtgtttggga 120

gagattccat aacgtcattg cctctgctac acatcattca ttggttccaa taatgaagcc 180

acgtgctaag gacattgaga gaatcttata aaacaagaaa tatagtaaat tgggaaatgc 240

attttatcgt ctaacctgct ttcctgaaag tacttggaga aacaaaaact tgctattaaa 300

tggctcaaac aaccttgata aatgccgcag aacttaattt ctgaaatttt tgcaaacatc 360

aatagcgcgc actcttcaaa tataaaacct tggagaagtc tgtatagcag ctcacatggt 420

cattcttaat tcacaccatg caattattca tccctttact tgcaagaact ttataactat 480

tctggttcac cgatgcagtt gttatctcaa cgtttcccat tgtatgatct ttgaaaatat 540

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agataaagtt actcgtttgc acagtagctc catattctgc aaccttcaat tttggatact 600

gaaccacttg cacattccaa tcatgtcttt taacttcagt gtttaagagt atgcttagtt 660

ttacaaactt ttaaagtctt ccctagctgt aacggtcac 699

<210> SEQ ID NO 165
<211> LENGTH: 620
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 165

aggtgaccgt aaaataccat gagaaatgct ttcatcaggc accgctggta ggttttctta 60

agcttttcat taggcaaaag aggctccgtg agttgatcgt taattctctc cttgaatgcc 120

atattgacca gacactctga ttagaaactg gaatacaact gcacatatag tcattctata 180

tgattcatcc ttctgcactt cagcatcctg cggcaactct tcatcccgcc atactgagaa 240

aaattatttg actcttgatc atgtgtagat gaatcttcat gaatcttctc atcttcattc 300

ttgtctttat atctttagga agtgcatctg gtaaaagtat aaatgcatct tcacgggtgc 360

ttcagttttt gcatgctccc ggttcttctt gtttagcatg tggatctagc aaatcactaa 420

atgtagttct ctcaattggt ctggtggaaa ttctcctcaa ttcgagaatt acgaatcatc 480

atacctgagt aatatatgtt gccctgtaca tgcatatgct ggtttttggc tccaccattc 540

tccaaagggc tcaaaaacta tgcgacccct ggttgccgta gtggaaggtt atacattgcg 600

ttcccagtag ccacggtcac 620

<210> SEQ ID NO 166
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 166

aggtgaccgt ggaggggctc cacttatatg catagatgat gctgcgaggc tgtgttcatc 60

tggtccaatg gagaagggga agaccaagtg cctatcctga ttttggtgcc gcttgttctg 120

gtgtacagaa tatcaaccca gggtatgtac catcacttcg tgagacgttc acatttcccc 180

acttcttggt ggagctggtg gaaagcctgg aacttcatca atctatcgtt ggtgtgagga 240

tgatcaggct ctgtacttat atccacatgt agtgcagcag gtggtggaga tgtctctgat 300

aagttggggg ttgatactgg ttcgtatcat ttgcagtgat gttcccccgc tgcccttaat 360

tgctattgat ccatcattaa ctataggttt ttactcgccc ggaataagac aatcttttga 420

cacttgttgc ttgggtcac 439

<210> SEQ ID NO 167
<211> LENGTH: 289
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 167

aggtgaccgt ggcgcctgac ctgtgcagaa tccattctca tggatacaat actgttaagt 60

ttgctttgct ttgcttgaag gatctgaatt gaaaaattgt ccccacaatt ctgtttcgtt 120

aaaaatgacc tcaatcactc tcgacagttt ccagatcttg attgggagcg tcctctcctc 180

tctcaagatg ttgttgacca aattcagggc gacttgtggc cagaaatcgt acattctgcc 240

atctacctgt tattgagctc cccgatttat atgcgctttt gacggtcac 289

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<210> SEQ ID NO 168
<211> LENGTH: 314
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 168

aggtgaccgt caataccatt aaactgggga ttcgtctcaa caagtcaaca tgctaacctc 60

acagctccaa tcaaacaacg tccgtcgaag ggcgctcaca ctcatccaaa ttacttccct 120

ctgcaagact cacaaaatca gattcttcat gaattgctca aacgaggctg ttatggatga 180

tgcagctgat tactcaagtg acagcactct gaatccccgt cccatatata gcgacgcggc 240

gtttcagccg tgactggtcg caacagcctc agtgggacaa aaggccagaa gccccccaag 300

gttctcacgg tcag 314

<210> SEQ ID NO 169
<211> LENGTH: 242
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 169

aggtgaccgt gtcgatgttg ttagatgtga ttagggtttt atttcttgat acagatgcac 60

tgtttctctg tttattcttt tatttcttca atgtatgttg tcaaattata cttagtcaga 120

tctccttta tcgttcgtca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagtttaaca 180

attaaaaggg gaaattaggc catatcagct tgtcgtatgg acccacatgc actgtaggtc 240

ac 242

<210> SEQ ID NO 170
<211> LENGTH: 195
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 170

aggtgaccgt atgcagagtc aaggtttagt tccttcagag cctgcccgag tagcactgag 60

gcagctcaag ccatttcacg taggaagccc acaacaaaat agaaatcaga gtgagtcttt 120

gatcgagtaa cccataagtt cttagctccc gttccatctt aacataagca tttttcttcg 180

tcttctcgca gccgt 195

<210> SEQ ID NO 171
<211> LENGTH: 217
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 171

attgcagagg acttagagag ggaaaaccgt tccgatctgg tgaagcaatt ggatgaagcg 60

ctctggaatt gattcccgtt tctgatgata tcgtacggct aagctcagct cttcaggcat 120

tggcagacaa tacgattctt caaatgagat gacagatttt aagaaactta taggatgaca 180

tatttcctag cttgaagcgg attcccccta cggtcac 217

<210> SEQ ID NO 172
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 172

aggtgaccgt ccgataaagg atgagaatat aggtagatca acccaaaaac actctcagaa 60

-continued

aacgattaaa gcctaacccc aagatcgttg agtaaattta acccggtaac ctccacataa 120

aatatactta gcaacaataa actcaacaac taaactatcc ctttaaaatt aaattatcct 180

tatttattta aaaaaacaaa tcctttatat actaaggtcc cctgcacatc tattactaag 240

gtaaaggaag ggaattatat gctatcattg taaactttga cttccgtatt tatgatcaga 300

ccatgagttt gataattaat tttacgctct ttactcccca ttcaaggcac gtgcctggtg 360

atatatgaac gccaaattat t 381

<210> SEQ ID NO 173
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 173

aggtgaccgt agaatacaat ctatgtatca aaatgctaac aaagagaatt tgttgtctag 60

cttgtaaata tacaaaagaa actctcacaa ggagtgagaa gcactaaggc ccttggaaag 120

aatacgtttc tattcagcgg agtgtatttt gagctacggc ttggcacaac tcatcctata 180

aaacaagact ctgtgagagg gcagagacct tgatcctggg cgtggcaagc cgggtgccta 240

ttgcggtaaa atcgagaagg gggaccctgg aaaagagagg ctgaaatttg tttcattctg 300

caactgaaac ctaaccggag gccgaatctg atcatttcta agacctttgg ggtcctgggc 360

atcccattaa aagaacgctg ctaactctcc cctccacaaa gggccaatgc gctcaggtcg 420

ggcttctcat cttcacattt cttgccgaaa tctatctgaa tttgttgtat tgaataacac 480

tgcctcctac acggtcac 498

<210> SEQ ID NO 174
<211> LENGTH: 604
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 174

aggtgaccgt gggcgccgtg gctcaaaagg ccctcgcaga cgcccgctcc atcaagctca 60

tgggcccccc ccaccctcgg ggggcaagcc gggaacgttg ctgtcagacg aggcgaggac 120

ctggaactgc cgttgaagga acggttctat attcagcccc tctcggcgga ccaggcgctg 180

cgagagccaa ggaatccgcg gaagcaaatc ctggaggtga aaaagctgat agataaaagg 240

cgtggccgta cgtccagaac gacctccgct ccaaggcttc ttaccttcgc tacgactcaa 300

caccgttatc tcctcaaagc ccaaggaaca gaaaaaaccc ctcaaaacct caccccaaag 360

ctttttgac acccttgaca aacctggact acgctgcaag gagccaagga taccccaagg 420

gcagaaaaaa tactttgcag aagctggtga accgcccttа atgatgttca ttccaagctt 480

ggttaagctg tattgcactc attgttaacc acacttaacg ccaatccaat ctatgctgtg 540

ttgcatctcc acttcttagt taataacgtt ctgtgttccc aaactctgtg ccacacacgg 600

tcac 604

<210> SEQ ID NO 175
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 175

aggtgaccgt acaatacaaa taggtagttt atcacattgt agcttataga atgtacaatt 60

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gaaatcaaat aaattcaacc aaactcaaat aatatgatca tgtgctcctc accttctcag 120

caaactcgta gagcagaaaa aaggattatg ttaaatcaca gttcacacat tagggtaaat 180

cccactaaat gacctctctt cattatccaa gtatctgaca ccaacatatt tcaaacaaat 240

agtgcaaaaa ggaatggtga agtaaaatag tcaaaactaa aaaataagct taaaatttct 300

cacatgtttg aatatgtgca ccacaaattt tgttagtgtc atcaaaatgc atgtaatcaa 360

cttgccgtgt atataatttc acacaatatc cgtaaaattt tgcaattcct tatgagcatt 420

tcatgtctag agattgcaat gacttggcta caaacatgtt tctctacaca agatcacaat 480

atttagtcag gacacgaatt gcaatgggga ttctcacaag catcacaagt catctcccat 540

gtactaaaaa attgtttaaa t 561

<210> SEQ ID NO 176
<211> LENGTH: 382
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 176

aggtgaccgt atagtgcata ttcagattgc aattacagac gtattagaac cagattttcg 60

cttcgataca gctcatcgag agcaacagag atccagatca aaaaccagac acagtttaag 120

aacatcgaaa taccaagccc agggacagtt accagcatat agctctacca ccaacagatt 180

attacagaac caaaacataa gaccacttgc agacaaaaat aaaccctaac gcagaacgtg 240

gcaactatct cctccagcta ccaccatcgg aaccaccacc accatagcga gaaccccacc 300

accaccatag ccgccaccgc caccaccata accaccacca ccaccaccac tgtaccgcca 360

ctaccgccat aaccacggtc ac 382

<210> SEQ ID NO 177
<211> LENGTH: 196
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 177

aggtgaccgt ccttggagat accagcttca aaacctccag tggtggagtc gatgatcaaa 60

ctgcacagtc agcctgagat gttccagtaa tcatgttctt gataaaatca cgatggccgg 120

ggcatcaatc acagtgcagt agtatttagt tgtctcaaac ttccagagtg caatatcatt 180

gtgataccac ggtcac 196

<210> SEQ ID NO 178
<211> LENGTH: 141
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 178

aggtgaccgt atagtaggaa ctttaggtgc tttggtggca ctctccaatt ttcatgtcct 60

tacatacccc actacggaga agggtagccc aagatttgaa cccaagactt ccggttcgtg 120

agacttcatt tccacggtca c 141

<210> SEQ ID NO 179
<211> LENGTH: 478
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 179

aggtgaccgt aagatcaaga gcacagaaag cagccatagc cccgcccatt gaatgcccat 60

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aacaataatc tgtaacccat ctctctgttt ctgagctttc tgaactgctt ctacaacagt 120

ggtcgtaagg ttgtgttgtg ataagcagag taaaatccat aatgtaccat tgcaccagca 180

tattaggata gttgagatca agtgtcttac agaataaatc ctccacccaa ttctgtagct 240

cctttcttga gtacccctga atgcaattac aattgcattg atatcttctg ccacaccaca 300

aaagcctgaa ggcagtgttg tacatcaact ataagctcta ccacctgaaa accccagtca 360

aaccattgca cctagaacaa gtccaagaca ttagagcact caaatcatcc ataagaccgc 420

agaagcatat tgcacaagta tctcagcaag tgttcgatta tagacatggc caggtcac 478

<210> SEQ ID NO 180
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (58)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 180

aggtgaccgt gggaggggag atttttgatt tatatttcca atataaaaga aaatctangt 60

tgtaaggaca tggcaagagc tcttatttcc ggggttttag ccgtggcccg gagcggatga 120

aagcaaatgt aagtcactcc gtgctttctc ggcatttgga cgcttctact ctaccgcact 180

acagacggga ttgaacctcg catctctgag tgtttggtcg tttacatggc ggacttgttc 240

cgcacctctg cggacgtcaa atgccgcgac gataatccct ttgagaacag cgatacggca 300

gaaagatcgc cgttgacgaa gcgagaaaac tattgagact tgcagatgtg gagctgaaga 360

agagcttgag tcgacggtca c 381

<210> SEQ ID NO 181
<211> LENGTH: 521
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 181

aggtgaccgt ccgttcgggg tgtattgtcg aacacgtagg atggtgctac gttgaaacca 60

ccgttacctt cttcgatatg ttatagttcg agttcatacg gagggaatac cgtttgtagt 120

gttattcagc acaaccccgt cctgattaaa caccccgca accaaggacg tattcgacgt 180

tcggtattgt ttgacacact caagttataa ccctgaatag gcgctacccg aagtaagcat 240

tgtaccagtc gttatttttg ccttcgtatt gcgaaggatt ttgaaatata tccggacagg 300

ctgcaaccga tcttcataaa actctttctt aaactgagca aactgaacag cattagcatt 360

ttgacccgac ctttcatcgg cacctgctgc acacccgcat acgtattaaa gctatgttcg 420

tctggccagg tttgcctttt ttggttgtaa tcaggacaac gccgttagcc gcccgcgatc 480

cgtagagcga cgtagaaagc cgcatctttc agcacggtca c 521

<210> SEQ ID NO 182
<211> LENGTH: 307
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 182

aggtgaccgt gaaatatgtg ggagatgata tgtggtttcc tgaatattca cctcttgtgt 60

agaaaagtga gatccttaag atgttttgct aataagactc ttaggaatgt tggacccctt 120

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tcagaatgcc atttgaatag attcaaggtg gtagctgttg cctggggctg ttttagggtt 180

ttaggccatg ctctgtaatt tcattgagtc aaaattggat taactggtgt cttttacctc 240

ataatagcta ctgcagtatt tgtcgatata gcttccctat ttattgactc tccttaggta 300

cggtcac 307

<210> SEQ ID NO 183
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 183

aggtgaccgt ccgttcgggg tgtattgtcg aacacgtagg atggtgctac gttgaaacca 60

ccgttacctt cttcgatatg ttatagttcg agttcatacg gagggaatac cgtttgtagt 120

gttattcagc acaaccccgt cctgattaaa caccccgca accaaggacg tattcgacgt 180

tcggtattgt ttgacacact caagttataa ctctgaatag gcgctacccg aagtaagcat 240

tgtaccaagt cgttattttt gccttcgtac tgcgaaggat tttgaaatat atccgcacag 300

gctgcaactg atcttcgtaa aactctttct taaactgagc aaactgaaca gcatcagcat 360

tttgacccga cctttcatcg gcacctgctg cacacccgca tacgtattaa agcaatgttc 420

gtctggccag gtttgccttt tttggttgta acaggacaac gccgttagcc gccgcgatcc 480

gtagagcgac gtagaagccg catctttcag cacggtcac 519

<210> SEQ ID NO 184
<211> LENGTH: 629
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 184

aggtgaccgt cgtcagaaaa aacgtgattt ccgcaaactt tggatcactc gtatcaatgg 60

gcagctcgtt tgaacggact ttcatactca caattgatgc atggtttgaa gttggctgaa 120

tcgaagtgaa ccgtaaaatg ttggctgact tggctgttaa cgatgcagca gctttcaaac 180

tcttgcagac gcagctaaag ctaagcttgg gtaaataatt aaaaaaagaa ccgaggtttc 240

cttggttctt ttttataact tttaatgaaa agtatgaaga gagaaacagc ctgtcttcta 300

cttatagtat aagataaaag cttgttactg ataagacagc tttcatggta aagcagttaa 360

aaatagggat ttgcgatata atagaaaaaa cagacgttta tgtaaataaa aaacagtaga 420

atggagaaat tatgtcagag aatcgtttgg cttgggatca gtattttgcg gccaggctct 480

cttaatcgct aatcgctcaa cctgtaagcg agccaaaggt ggctccgtat tgtcaaggat 540

aataagggtt atttcaactg ggtacaatgg ctcagtttca gggactggag actgtattga 600

ccaaggagtg cctggtcatt gacggtcac 629

<210> SEQ ID NO 185
<211> LENGTH: 413
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 185

aggtgaccgt ggcggaggtt agggaagttt gacttctcat tttctcacgc actcctctcc 60

tcgtaacctc ggtcgagtcg atggcggctt tttagtcgag tgtgctaacg caccctccgg 120

cctcaaaatt tccagctact cgtatttgat caatgctgaa atcgcgtaat tacgtagtaa 180

taaagcgtaa tgaattctat aatgaagcat gtttctctat agttcatgtg ccgagaggaa 240

-continued

taatgaaaat gaggccttat atattatctg gggctcaagg agatgttatc ttttccttcc 300

ttggttagag accgtcaacc ttcacttgat tggataaagc ttcattttgt taaaacctcc 360

aagccagtag atacatacgg taggcacgta ttatggtaga gacatacggt cac 413

<210> SEQ ID NO 186
<211> LENGTH: 397
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 186

aggtgaccgt cctgttgcct aaccgcgaat ccaaatcgac ttgggctgct tcctttcgtg 60

cagatatttc tggtttggac tctagttctt gctcctggaa atcatgcttg agtgctgggt 120

agctgcctcc aagtttggtt gacaggccca ttccttacag cttctctctt ccgcttatga 180

cagagtaatg acaggaattc aacctgacgg atccgtctag ctctcacaag gttgggaccc 240

tgtcttcgag agggttattt cttgagactg ttgactatat tttggatgag ccctcagctc 300

tgtgtactat tgttcatgta ctggatactt tgtaaatgat tttattctgg ttttaccccg 360

gggggggcat tttgactcct gggtttaata cggtcac 397

<210> SEQ ID NO 187
<211> LENGTH: 467
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 187

aggtgaccgt ggaacatgat gattagttct tctgtgggcc aggatgatta gttctctgtg 60

tgactgtggg ccaggatgat tagttctcct gtgacgactg ttggatagga tgattcgtct 120

cctgtggaca ggatgattag ttctcctgtc gaggcaccct acccatgcaa tttgggatca 180

tgggaagtac ctctcatctg atcaatgagt agggaaatgg ggttagggac cattagagta 240

ctatcgatgg acacatcgtt gtatctaccg tcctatgcta ggacgacctc cattgtttgg 300

gattagtgag agtggtatga cactctgaga ctgactttgg gtcagtggag gatgtatgat 360

acatcctcga tcatttcttc ttcttcatag ttcgagcaga gcagagcaca acaggccaag 420

tagtgcaggg tagtgcattt gatggctggg atagtagcga cggtcac 467

<210> SEQ ID NO 188
<211> LENGTH: 555
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 188

aggtgaccgt aaataagatg acccacatgg agtttggccc tagtttccaa ttttaacacc 60

gctctcaact agggagaact ccattcgctg atccatttgt ccgactatac tatctctgca 120

tcagtgccct acactactct gcactgctct gctctactaa accatgaaga agaagaatga 180

ccgagaatgt ctcatgccat tctctattga cctgaagtta gtcctatatg aagagatgtg 240

tcatatcact cttattgacc caaagtcagt tttattgatc ccagatcaat atcacagaga 300

gtgtctcaaa ccactcatac tgatcccaga tcagtttcat tgatcccata tcaaggagat 360

catcctagaa tagggagtac agtagataca atgatgcatc catcaatagt actctatggt 420

ccctaacccc atttccctgc tcattgatca gatgagaggt acttccgatg agcccacact 480

gcatgggtag gatgcctcga catgagaaat aatcatccta tccacaggag acgaatcctc 540

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ctgtcccacg gtcac 555

<210> SEQ ID NO 189
<211> LENGTH: 695
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 189

ctagggaaga ctttaaaagt ttgtaaaact aagcatagct cttaaacact gaagttaaag 60

acatgattgg aatgtgcaag tggttcagta tccaaatatt gaaggttgca gaatatgggc 120

tactgtgcaa acgagtaact ttatctatat tttcacaaga tcatacaatg ggaaacgtga 180

gataacaact gcatcggtga accagaatag ttataaaagt tcttgcaagt aaagggtgaa 240

taattgcatg gtgtgaatta agaatgacca tgtagagctg ctatacagac ttctcaaggt 300

tttatatttg aggagtgcgc gctattgatg ttgtgcaaaa atttcagaaa ttaattctgc 360

ggcatttatc aaggttgttt gagccattta aatagcaagt ttttgtttct ccagtacttt 420

caggaaagca ggttagacga taaaatgcat cttcccaatt tactatattt ctgttttaaa 480

agattctctc aatgtcctta gcacgtggct ttcattattg ggaccaatga agatgtgtag 540

cagaggcatt acgttatgga atctctcacc aagaacactg ttttgggctt tagatagctc 600

ctagttataa atgctccagt gacaaacaca tcctaagttt ggggcaatta atgacgcctt 660

ttggtcattc tcctttgggt ttcaggcacg gtcac 695

<210> SEQ ID NO 190
<211> LENGTH: 144
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 190

tccctttagt gagggttaat agatctatag tgtcacctaa atcgcggccg ctctagaaca 60

gtggatccgc aagcaggata gacggcatat gcattggatg ctgagaattc gatatcaact 120

tatcgatacc gtcgacctcg aggg 144

<210> SEQ ID NO 191
<211> LENGTH: 185
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 191

ggtgcgatcc taaacatgca agctttgagt ttgtaacttt gtagaagtgg acatttctaa 60

gttggatgta caaatctact gttggttgta ttgtcatccc ataaacaact gtttgatgag 120

atgtttttttt aaaaaccaca tcataatatt tttaggcctt gtaaaaaaaa aaaaaaaaaa 180

aaaaa 185

<210> SEQ ID NO 192
<211> LENGTH: 167
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 192

attccaaact tttctttcaa gatgtacacc aacatcattg tccccaactt agtagacttg 60

acttttcacc aggtccaaag agaggggtgg tggaagcaga tttcaggctt tcgaataagt 120

atcaatgata taagcatcat ccccttgcca attgttctgg atcgcac 167

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<210> SEQ ID NO 193
<211> LENGTH: 167
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 193

ggtgcgatcc catcaggggt tgtgtttcta agaatcactt ccatgtttca aattcagcac 60

ttgatcttgt acatacccaa tttgttgcct gctactagct agtattgtct ttcagtttga 120

accatttttt tgagtaaatc gtgtttagtc tttggcaaaa aaaaaaa 167

<210> SEQ ID NO 194
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 194

ggtgcgatcc gcattagaga agcatacagg aaaaagaagt acctgcctct tgatttgcgc 60

ccaagaagac tcgtgctatc aggcgacgcc ttaccaagca tcaggcatca ttgaagacga 120

gagacagaaa aagaaagaga tgtattttcc aatgagaaag tatgcagtca aggtgtaagc 180

cacaggattt gagctttcat gcaatttttt tgttacttgc gggatgatat tgcctatata 240

tttccgtcca cgtttttggc aaattccgat ttgcatcaga attcaagtta tgatagtgtt 300

ctttcgcttt tgagcagttg atattgttta tcttttattt ctcttgaatt gcaacatatt 360

ctaatgcaat gagtggatta ttatattgtg gtatttccat gttgaactca tataaatgag 420

cgtaatttga gtggtagcgc taggatattt acacttggca aaaaaaaaaa 470

<210> SEQ ID NO 195
<211> LENGTH: 289
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 195

ggtgcgatcc gtataggtag tttggatgat gaacgggcaa agaaggcaaa ggagtacagg 60

atggatcctg taattcctgt ttcagaaaac agaaaatctg caatataagg atggctaact 120

tttcagctat gaaaatatat ggtgcagtgg cactcatatc agttgcagag ttgtcaaata 180

acttttgtga ataggaaagt tgtcctcttt tagagtgcag aaatcctgca atataagatg 240

gctaagtttt tcagctatat gaaaatatat ggtgcagcaa aaaaaaaaa 289

<210> SEQ ID NO 196
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 196

ggtgcgatcc catatacaat tacatatatt ttcaacaatt cttttgttgt tatgaaaatc 60

tattgaaata aattgaaata gtttgcatca tttatttatc ggaattcgta tttatatatt 120

aaatttctga tgtctcaaat ccttcgttac tgtaacgata tcattaatat aatgtgtctg 180

caagtttatt gggcaaaaca aaatttattt ttcggtcaca tcataagttt atttttggtc 240

acatcatatg caccatcaca ttaagcataa gcatatacag tagcgtaaaa atacaattat 300

tgttgttgac taggatcgca c 321

<210> SEQ ID NO 197
<211> LENGTH: 188
<212> TYPE: DNA

-continued

<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 197

ggtgcgatcc tagtcaacaa caataatatg tatttttacg ctactgtata tgcttatgct 60

aatgtgatgg tgcatatgat gtgaccaaaa aataaactta tgatgtgacc gaaaaataat 120

tttgttttgt ccaattagac ttgctgtata tgtctggagt cctacccttg aaaattgact 180

tgtttccc 188

<210> SEQ ID NO 198
<211> LENGTH: 145
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 198

ggtgcgatcc catatacaat tacttatatt ttcaacaatt cttttgttgt tatgaaaatc 60

tattgaaata aattgaaata gtttgcatca tttatttatc ggaattcgta tttatatatt 120

aaatttctga tgtctcaaat ccttc 145

<210> SEQ ID NO 199
<211> LENGTH: 151
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 199

ccactgcacc atatattttc atatagctga aaaacttagc catccttata ttgcagattt 60

ctgttttctg aaacaggaat tacaggatcc atcactgtac tcctttgcct tctttgccgt 120

tcatcatcca aactacctat acggatcgca c 151

<210> SEQ ID NO 200
<211> LENGTH: 254
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 200

agagccttct tgcagacaat ccgtgaaaac atggctatac aataaaaatt cccagtttga 60

attctaaaga aaactgttca atatttgaag gcctctgata tcacagagac tgatattaaa 120

tggaaattca tacaaatgag gagagcatgt agcaacacta gaagctttgg cataaagcac 180

cagataaatt cataagaact aaatccataa gaaggatctc tcgttcacca gtcacaatca 240

cactcggatc gcac 254

<210> SEQ ID NO 201
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 201

ggtgcgatcc ctggccctga taactttggt tgcaatggaa aatgcagtac taggtgcgaa 60

atgctaaagc ccgcccggag cggtgcatga agtactgcaa tatttgttgt agtaaatggc 120

tggttgtgtt cccagtggtc actatggcaa caaggacgag tgcccctgct acagagaatg 180

aagtccgcag ccggcaagcc caagtgtccc tgatcttagc acttcagtcc agtcgccact 240

tcttttattc tctttttttа taaaagtgac gaggccgttt ttcttgtgct tggtgccata 300

tgtagagcgg tggctacttc tcctgtgtta ggaaatgttg cagtactaat aatagaactt 360

ctt 363

-continued

<210> SEQ ID NO 202
<211> LENGTH: 162
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 202

ggtgcgatcc aataaagata tactttgcaa caataatcaa aatatcatta tgcaaagttt 60

aagatcaaaa tagaatgcaa caaaaaaatg gttgtaacat aggaaccaac aatgttgcat 120

tcaagtaaga ctctttgcaa aaaaaaaaaa taaaaaaaaa aa 162

<210> SEQ ID NO 203
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 203

ggtgcgatcc acaagtaaga taattgagta tatattcaag atgcaaatat ttcattagga 60

ccactcataa agttatcaat gattcacaaa gagacctcct gacctctctc aaaagtggtg 120

gcaacacaag actagtgtag tttttactat acctcaatga aactaccatc ctaactgatg 180

ccataatctt ctgttatata ttaccaaaat ttatgagatg attgatccat aaacactcca 240

gaacacatag tcatccaaag gaacctttgc ttgaatatgg acccccttaa ttcaggtact 300

tgctactcca ataaattgct taatctctcc accgataacc acagtttgga tcgcc 355

<210> SEQ ID NO 204
<211> LENGTH: 297
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 204

ggtgcgatcc aggacatgag gccgagtttg ccattgtgat atgattgagg aagtccagtc 60

tcaaaattag gtttatcttg atgtttgaca agaaatatag aagggcatga tgaatcaaga 120

acctttttcca aatctgttac tgcaaccaat ccaatgacat aataacgcca atggttggtt 180

cctgtgatga cataataaat tggattaaat taataacatc cctaatgcca tgtggttagc 240

tgcatcatca ccgtatccat cgagtgttca atttttggga tgtatgtatc aaaaaaa 297

<210> SEQ ID NO 205
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 205

aaatattttt caatacaacg ccatgtgaca tttttgtgct tcttgttttt gatacatact 60

tccaaaaact gaacactcga tggatacggt gatgatgcag ctacagccat tgcattacga 120

tgttactaaa ttaaatcaat ttattatgtc atcacacgaa cccaaacaat agcgctatat 180

gtcattagaa tggttgcagt tacagatctg gaaacagatc aatgaatcat catgccctct 240

atatctcttg tcaaacatca agataaacct aattttgagg actggacttc ctcaacatat 300

cacaatggca aactcggcct catgtcctgg atcgcac 337

<210> SEQ ID NO 206
<211> LENGTH: 344
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 206

ggtgcgatcc gtataggtag tttggatgat gaacgggcaa agaaggcaaa ggagtacagg 60

atggatcctg taattcctgt ttcagaaaac agaaaatctg caatataagg atggctaact 120

tttcagctat gaaaatatat ggtgcagtgg cactcatatc agttgcagag ttgtgaaata 180

acttttgtga ataggaaagt tttcctgttt tagaatgcag aaatcctgca atataagatg 240

gctaagtttt tcagctatat gaaaatatat ggtgcagcag agttgtcaat ataaacttgt 300

gaatagggaa gttttggcaa aaaaaaaaaa aagaaaaaaa aaaa 344

<210> SEQ ID NO 207
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 207

ggtgcgatcc tcgttgtgaa gacgtagtga tggaaaggtc atgtttgtag gagacataat 60

tataggagtt tctttattat aataaccaag aagtccgatc ctgggggcgt tgagtatata 120

gtcagtcttt ggtaatttgg tgtggtgctg tttgacctgc ctttcctttg gagcaatgat 180

ccttgaggat ggaagaggtt atgttgaggc tcaagagatg attgtttgag ttgtggaaag 240

caaaaggttt ccagatgtag tcagatagta acttctatgc ttttaataaa atttagtctg 300

tggggcatgc ccctttttgc tggcaaaaaa aaaaaagaaa aaaaaaaaa 349

<210> SEQ ID NO 208
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 208

ggtgcgatcc gtataggtag tttggatgat gaacgggcaa agaaggcaaa ggagtacagt 60

gatggatcct gtaattcctg tttcagaaaa cagaaaatct gcaatataag gatggctaag 120

cttttcagct atgaaaatat atggtgcagt ggcactcata tcagttgcag agttgtgaat 180

ataacttttg tgaataggaa agttttcctg ttttagaatg cagaaatcct gcaatataag 240

gatggctaag tttttcagct atatgaaaat atatggtgca gcagagttgg aaaaaaaaaa 300

aaaaaaaaaa aaaaaaa 317

<210> SEQ ID NO 209
<211> LENGTH: 389
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 209

ggtgcgatcc caggagaata ttagtttcat gtgttgctat cattttcttc aatatgcagg 60

gcaaccattt gaatgaaact attcctttcg aatttcaaaa acttaatagg ctaacttatc 120

tatctggagc cgattttcat tgacgagtaa cctgtaagct ggccagcaaa agccaacaga 180

tgttcagctt gttggaacca gttgaagatt gtaatagaga tggtgaataa tcgcggacgg 240

ctcggccaat ggaatatttg ttgcatcatc atcaaggggg tatgaattcc aaagaacttg 300

ttgattgaaa ttcccaagca aaattctgtg aaatgaaaaa tttattgaga ccattgggca 360

aaaaaaaaaa aaaataaaaa aaaaaaaaa 389

<210> SEQ ID NO 210
<211> LENGTH: 242

-continued

<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 210

ggtgcgatcc gactgtgata tgtgactggt gaacgagaga tccttcttat gaattaatct 60

ggtatcttta tgcgaaagct tctagggttg ctacatgctt ccattctaat atcagtctct 120

gtgatatcag aggccttcaa atattgaaca gttttcttta gaattccaaa ctgggaattt 180

ttattgtata gccatgtttt cacggattgt ctgcaagaag gctctttggc aaaaaaaaaa 240

aa 242

<210> SEQ ID NO 211
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 211

tttttttatt ttttttttt ccaacgagat cactgtcatt gttcaataac tatatgccaa 60

agagccttct tgcagacaat ccgtgaaaac atggctatac aataaaaatt cccagtttgg 120

aattctaaag aaaactgttc aatatttgaa ggcctctgat atcccagaga ctgatattag 180

aatggaaatt catacaaatg aggagagcat gtagcaacac tagaagcttt ggcataaaga 240

caccagataa attcataaga actaaatcca taagaaggat ctctcgttca ccagtcacat 300

atcatactcg gatcgcacc 319

<210> SEQ ID NO 212
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 212

ggtgcgatcc gactgtgata tgtggctggt gaacgagaga tccttcttat gaattaatct 60

ggtatcttta tgcgaaagct tttagggttg ctacatgctc tcctcttttg tatgaatttc 120

cattctaata tcagtctctg tgatatcaga ggccttcaaa tattgaacag ttttatttag 180

aattccaaac tgggaattta ttgtatagca atgttttcac ggattgtctg caagaaggct 240

ctttggaaaa aaaaaaaata aaaaaaaaaa a 271

<210> SEQ ID NO 213
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 213

tcccaaaggc aattatacat ggatcgcacc 30

<210> SEQ ID NO 214
<211> LENGTH: 517
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 214

ggtgcgatcc ccactgcaga aagatgagcc agtaccctga aattttgctg ttgtccatgc 60

ctgggtcacg gaggaaagaa cggcacggtg caatatgatt ttgctacata caagttccaa 120

gagtggatgc agacagtgct ggccatggct gattatttgc aggtgactaa tgctcttttg 180

gttatcctta ccatcatcat cttcctgcca ttcttttgta cctcggtatg gagacgaaca 240

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cccacttttc aaagtttgca gaggaagcat gtattcataa caggaggatc aagcggcatt 300

ggccttgaga ttgccaaaga ggctctttca cagggttctt acgtgacact ggcgtcaaga 360

aatctttcta aacttcgtag ggctgttgaa gaaatcatcc aagaagtgga gtgcgacgga 420

gacaagatta atatcaaggt aatataccct gcaaaatgtt gtctggaata caatccaaaa 480

ccaatttagc aattaaccca ttggcaaaaa aaaaaaa 517

<210> SEQ ID NO 215
<211> LENGTH: 734
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 215

ggtgcgatcc aagtgcggta ttcttccttt ggcagttctc tgaactgttg agagaatttg 60

agtaggataa cgacaataat tactatgctc acaagcccag acaacacgaa tagactccct 120

tccgtgcgtc gccttccaga ggacgcagca gctaaaatct cggcctgact caccacatat 180

atatttaata gcttgtatat gccatatgaa ctgttagcat gatctccctc taactgcgaa 240

ttgtgttgct gtaaactaat cccaaaggat gtttactctg ttgcttttcc aactgctgat 300

ggatttcgct catacaatga cccgagagca ccataaacct acccagcgtt gtggcctatg 360

acccatagct ttttgttcgc acagcaattg aagaccggct acaggagatg actaatgcac 420

ttccgagaag gtttcaccgc gaatgacagg gaaggacaag gcagagcagc aggccaagac 480

agctttagtc gcagaagttc aagcagatct agattcatag taaatggaag ttctacacta 540

gttacaaatt taaaaacgta cctgcatgga ctacacggtt tatttacgag tgccacttgt 600

ctcattgttt tccatcagat gtctgctgga ttgtggtagt gtgttctacc gtatcggtgc 660

gggttttgta tattgtgcgt cgacagagtg acaggtggtg attttactgg caaaaaaaaa 720

aaacaaaaaa aaaa 734

<210> SEQ ID NO 216
<211> LENGTH: 664
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 216

ggtgcgatcc tagtacaggc gtttggaaca gagtggagaa tatgtggagt attgggggat 60

gcccccggtc gtgtgttgct gcgtttggga atttgtattt cttccatagg caacaagtga 120

tgtcttataa tagtaaagag aatgtttggg aagtggtggc atctcttcct ggagacatga 180

atattgttac tttgcgcaac agtgtggtgt gacaagatat ttgtgagcgg ttgtgcttgc 240

agtggcggcg atcaggtgtg ttacatgctg gacaaatctt gggcgtgggc tcctattgag 300

aggtcacatg agtttgaggg ttttgctcag tctgcaataa ctgtagagat atgagcaaat 360

tctgttgggt tcacttaatt ttgggattat tatagtgcag aggggagccg ggaagtttca 420

gtgtacagtg atgggcacca catgttgcca gcattggggg tgccctgtga atatgatttc 480

tataagtccg gattttaaat atctaggcca tctatctcat ccagcctctg attgtgtctg 540

tactaaatat atcctgtata ttcgtgatcc ctggttttga agtgagcaag ttttagtgga 600

agaggatttt tattaaatat atataaagtt tctgtattca gggttttggc aaaaaaaaaa 660

aaaa 664

<210> SEQ ID NO 217
<211> LENGTH: 422

-continued

<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 217

ggtgcaatcc gccataagag aggcatacag gaaaaagaag tacctgcctc ttgatttgcg 60

tcccaagaag actcgtgcta tcaggtgacg ccttaccaag catcaggcat cattgaagac 120

tgagagacag aaaaagaaag agatgtattt tccaatgaga aagtatgcag tcaaggtgta 180

aagccatagg atttgagctt tcatgcaatt tttttgttac ttgcgggatg atattgccta 240

ttatatttcc gtccacgttt ttggcaaatt ccgatttgca tcagaattca agttatgata 300

ggtgttcttt cgcttttgag cagttgatat tgtttatctt tatttctctt gaattgcgaa 360

catattctaa tgcaatgagt ggattattat attgtggcaa aaaaaaaaaa aaaaaaaaaa 420

aa 422

<210> SEQ ID NO 218
<211> LENGTH: 239
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 218

gcggacgcct caggatagcg ttagggttgc cttaggatag cgttagctct gccttctaag 60

gttgccgtct tatcctccag cgtctagggc ttccactcct aggatttctc ttccactaaa 120

acccaagaca agtggagaga aatcaagata gaagtgtgtg tgaaatgact cttaagtcat 180

ctccttttag actaaaacat tgagcacatg tggggtttat ttggttgctg gccgtcgtt 239

<210> SEQ ID NO 219
<211> LENGTH: 303
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 219

ggtgcgatcc tgaaacaaca tattcccgat ggctcttccg aaggaaccat tgctctactg 60

tgtggccctc cccccatgat ccaagatgcc tgcctaccta acctggccaa aatgaattat 120

gacattcaga attcgtgttt tcagttctaa ttacaccctt ctggttaatc aaattgggac 180

atcccctccc acatcctgtt attaattaag ccatagtcta gtgtataaaa tctgttgatg 240

tgtacagcat caagttaatt tcctccttttt ctgtcaaaaa aaaaaaaaaa taaaaaaaaa 300

aaa 303

<210> SEQ ID NO 220
<211> LENGTH: 273
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 220

ggtgcgatcc gatcctaagc gggtgcatat atataatgac aagctgtagt aactaactct 60

tgtcatgagg ccattgctaa catagcctgt ccaatgcaca tagcagtcaa aaaaagcaaa 120

tagccgccat gttcccatac acgaagtaag taccctccct attgagtcac cttacccgcc 180

gagagagatc ccaattccat gtattcggtt aagtaagccc tgccagctat gtcccaccca 240

tgaaagaaag tactgatccg agtggatcgc acc 273

<210> SEQ ID NO 221
<211> LENGTH: 364
<212> TYPE: DNA

-continued

<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 221

ggtgcgatcc aaactgtggt tatcggtgga gagattaagc aatttattgg agtagcaagt 60

acgctgaatt aaggggtcc atattcaagc aaaggttcct ttggatgact atgtgttctg 120

gaagtgttta tggatcaatc atctcataaa ttttggtaat atataacaga agattatggc 180

atccagttag gatggtagtt tcattgaggt atagtaaaaa ctacactaag tcttgtgttg 240

ccacccactt ttgagagagg tcaggaggtc tctttgtgaa tcattgataa ctttatgagt 300

ggtacctaat gaaatatttg catcttgaat atatactcaa ttgatcttac ttgtggatcg 360

cacc 364

<210> SEQ ID NO 222
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 222

caatctgtct gcaattgata ttattgcatc cagtaaacca gatacacatt caccacaaca 60

ttagagactc tagaagttcc tttggcgaca ggcaaaactc atgattacag ataattggag 120

tttcctctaa ccagagtcaa acgatctaaa gggatttgtc tagtcctcca ttccctcatt 180

caatgaggcg atggcttatg ccgtgacaac agtttctata gttgcatccg ctcctcttga 240

tcccacaaca tttttggtgt tctctgcatc ttcttcctcc catatctctg gcagggcttc 300

tctaatgttg tgaatacttg caagggcaaa atctgctccc tctgttcgga tcgcacc 357

<210> SEQ ID NO 223
<211> LENGTH: 222
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 223

ggtgcgatcc tctcagttac gagctcaatt tcgaccaggg gtctcggcaa attgaggatc 60

atgagaagca gggtatgccc ttgaatgccc tgaagccagg ggagtctcag ggcaatcacg 120

aatgaaacct gacaaaccct aagaaaaccc ctagagcgtg ccctgcagaa agggaattct 180

ttttgaggcc ggcggtcttt ctgtcgtctt ctcgcagccg ta 222

<210> SEQ ID NO 224
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 224

ggtgcgatcc agcaagagaa cgaaaaaggt atgagaatct atgaaatatt tgtacatcac 60

tgtattcata tgagggcctt tttttacaat gcggtagggt tgtttggaga attagaacct 120

gattaaaatg tagatggatt caagctttta gtgaaatgag gctcggaacg caagtatgct 180

gtccactttg agactcattc ttctatagta tctgaagcca aagcc 225

<210> SEQ ID NO 225
<211> LENGTH: 415
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 225

ggtgcgatcc catgggatag ttgcaaaaca cacaaatttg ttgtgaaaga agagagacac 60

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gcacagacaa ccatatgatc ttttttttt ttttttttt ttttttttt ttttttttt 120

ttttcacaac tctgctgcac catatatttt catatagctg aaaaacttag ccatccttat 180

attgcaggat ttccgcattc taaaacagga aaactttcct attcacaaaa gttatattca 240

caactctgca actgatatga gtgccactgc accatatatt ttcatagctg aaaagcttag 300

ccagccttat attgcagatt ttctgttttc tgaaacagga attacaggat ccatcactgt 360

actcctttgc cttccttgcc cgttcatcat ccaaactact atacggatcg cacca 415

<210> SEQ ID NO 226
<211> LENGTH: 229
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 226

ggtgcgatcc tgcgagagcc gagggttcat tttcctttcg acaacgacgt tcagtggcga 60

ccagagtttc ccaatcactt cagcgattct attccttcgt tgtaataaag cttaaggaat 120

ccatgcttta ttccttggaa ggtttgaata tttatatttg ttggcattaa tgctatatac 180

atctatacta attttgggtt gttctaaact tgttttgaat aacttaaat 229

<210> SEQ ID NO 227
<211> LENGTH: 219
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 227

ggtgcgatcc atggcaaaga gctcgttcaa gcacgatcat cctccagaga gaagacaagc 60

tgaagcttct cggattcgag aaaagtatcc ggacaggatt ccggttattg tggagaaggc 120

tgagagaagt gagatacctg atattgataa aaagaaatat ttagtcccag cagatttgac 180

tgttgggcaa tttgtttatg ttgtccgaaa aaaaaaaaa 219

<210> SEQ ID NO 228
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 228

ggtgcgatcc cctgtattct tgaaagggtt ataacggaag atagcatttt gctcagattg 60

tagacagtct gcatgatttg tcaatactac tatttcgcat tatttgttaa tactactaat 120

ccttgtactc atctagacta tttaattatt aaattctaca gtttctttct cctagatggc 180

aaacaatatg aataaaatgc caatagtttt ggaactactc cattaagagc tttagatgat 240

tatcattcat catttgcctg ttttgaatcg taaatgaatg tgtcacggtc ttcttttctg 300

ttagtctcta tgctttcatc agaagagtct aagccagtta ctggaagcta tttgtcatct 360

ctttaaacat tgtttccgtg ccaaaaaaaa aaaaaaaaaa aaaaa 405

<210> SEQ ID NO 229
<211> LENGTH: 329
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 229

ggcagaactt ccaaagtcta gtatttgatt aactaatatg atgaagacac tcagtctata 60

acatgacgcc agaaatcaga ccatatgcat gataactagc acgattaaaa tacaattcgc 120

-continued

aacctttaat acactaaaaa cgtttactgt atagtccact cagaacattt cgatagtatt 180

gtcagatcga cttatttagc tcatattcag caatctgaac tgtacgatgc ggctcattca 240

agggcatttg ggtttgccct tggcattctt catatcccga tagcaaggac acgcgttctt 300

gttgccatat gtccctgggg gatcgcacc 329

<210> SEQ ID NO 230
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 230

ggtgcgatcc acattggcca ggccggtatt caggtcggca atgcctgttg ggagctttac 60

tgtctcgagc acgacattca gcctgatgga caaatgccaa gtgacaagac cgttggcggt 120

ggagatgatg cattcaacac atttttcagt gagacaggtg ccggtaagca tgttcctcgt 180

gccgtgtttc tggatctgga gccaactgtc attgatgaag ttcgaaccgg cacatatcgg 240

cagctttttc acccagagca gctgatcagt ggcaaagaag atgccgccaa caactttgct 300

cgtggccatt ataccattgg taaggaaatt gtggatctgt gcttggatcg cacc 354

<210> SEQ ID NO 231
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 231

ggtgcgatcc cagcattgga tgcatttcta gcacaaagcc atcttgacta aaatagcact 60

gcgggcaact gcagtccata actttcagag cattgttgct gcctcaattg tataccaatc 120

catattctaa aaattagacc tggaaaccag tcagaaattt aatgttttct tgcagaaaat 180

gccctttag aaaaaggaga gaataactgc attcaagttc taactcccag acatagcctg 240

gcaacgtcat tcattcagtt cggatcgcac c 271

<210> SEQ ID NO 232
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 232

ggtgcgatcc agaaaacagc acaagcaatc tgtaagacca atattattat catctctcac 60

tgctcgtgaa caaaatgctg gttcatagcc atcacgaagg ctaaggctac tatccagcca 120

aactgatctc caacaataat ttcataagct taaataaata gtccatccag tggatggagc 180

cagaaagcca tagaaacttc aaatacttgt ggtatcaatc tctcctctgt taagggaggt 240

atcagatcag aagcactaat caaatgcata cataaatgca gtagactgca ataaaacaaa 300

atctgcagat agcaactgag cgcttaacga acggaaaaga gtttaacttg atctatcaca 360

ggatcgcacc 370

<210> SEQ ID NO 233
<211> LENGTH: 328
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 233

gaaaatggga gcctcaaata ttcaaagcct catctcaaga gtctcagatt cggattcatt 60

tcatttggtt cgtaataaaa taatgcatca aatagttatt atccacaaaa atgggagaat 120

-continued

tattacaatc tgtcttctca acataaagtc atagcatagc atagaaccac accacagtcg 180

tcatcatttg ttttgttcac caccgaaggg gctctttaca gcgtccatga agccctgtgt 240

agcacccttc gccttgtccc ccgcctgttg gaagaaagag ccagtttgtt ctttcccctc 300

ttgggctttt cccgtgatgg atcgcacc 328

<210> SEQ ID NO 234
<211> LENGTH: 157
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 234

ggtgcgatcc tattatagaa ccatgactct tgtcgatggg gcataaactt ctcattctta 60

ggcgtgccta ctgtgactct tgccgatgtg gcataaactg cttattctta gttgtgcctt 120

ctgtgcagaa cttgttgagt cggtggatta cactgac 157

<210> SEQ ID NO 235
<211> LENGTH: 334
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 235

ggtgcgatcc attaactaga ttaacgataa cattcctctg catccaatcc aatgctcatc 60

taaatctact tctacttaga tctctgcctc atctttctcc acctcctcat ccattctgaa 120

atattaattt ctgcatagat tttgttaggg tctagtaatc attttcatga atttaaatct 180

gttctagtct cttattatta tgctgcttat gctagcatca gaacctgtgt ataattcatt 240

catgtatata ttggattaca caaattatac ggatgccaga aaaaaaaaaa aaaaaaaaaa 300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 334

<210> SEQ ID NO 236
<211> LENGTH: 199
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 236

cttgaagctg atatgtttga acccgaaatt ttgttaccca actccagtgt acattgtgtc 60

actgtcaaag agaacatgag agctgcatgc aagcttttgc atgatagata gattactgat 120

caccgaacat ttcttactct actttcctct cctatcccca gtgatttttg ggcatttttct 180

ataccccttcg gatcgcacc 199

<210> SEQ ID NO 237
<211> LENGTH: 220
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 237

ctcatgaaca gcaatatgat gcattcctct tatacacatt tcatatatgt tcacccttgc 60

cgtcatggct actctaagaa gagcaaaaca gacccattga atctttacac gcgcttgttt 120

atatgaatac aaataattta ggcgtttctt tacacgccct tgtttacatt aatacaagtg 180

atttaggcgt tgttaccaga atagtgccac ggatcgcacc 220

<210> SEQ ID NO 238
<211> LENGTH: 555
<212> TYPE: DNA

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<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 238

ggtgcgatcc caagatagaa aagggaacta tggtctcgag gagtgtcagg tgctacagat 60

cacaatatac ataagggtct gatagtagta ctcggcccaa tgtttgaggg ctctaactaa 120

ggaggatcaa ccgtaccctt agccgtaaaa cccgactacc ctatcgtacg ggcgagtaat 180

ctctctgagt gttgttctcg gtgtatcgta gcagcaacac ggctgacggt ttatctatgg 240

tgaggtttca aaggagctag ggggcttcca atatacccag agggtacttg gaagacagtt 300

tatacgcggt tctgtctaat gcgctactac tcgaaggggt acccacaggg gttacaagag 360

agtgcaacaa gcatgaccac cccttgtatt tcttgcatgt atgcctcccc aaatccgcag 420

gtttatgcgc tcattgacag attccgtggt ttaaagatgc cggaacatgt ctctagccaa 480

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540

aaaaaaaaaa aaaaa 555

<210> SEQ ID NO 239
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 239

ggtgcgatcc tcctaacctg caatgtcctt cctgcaacct gcaattattc aacagaaatt 60

aggtttattt ttctttttgt cttttcttct ttttttttt ttttttttt ttttttttt 120

ttttttaagt aaacgaccat ttcaaacgcc atttcaaatg ctatgaatta atgttgaatt 180

aatgttagca ttaagtctta aacattttat gttaaggcat atatatcgtt ccaactactc 240

ttacaataca cctgcggtgt actcctgcca ccgcatgtac caccgttaca tgtacgcctg 300

ccagcacatc taacaggtgc caactccttt gaactcatcg tcgccatttt tgtatgcata 360

tttgaactca tcgtcgccat ttttggtatc ttcacatatg gccagtccag gatcgcacc 419

<210> SEQ ID NO 240
<211> LENGTH: 129
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 240

ggtgcgatcc aaggagtggg cgtgcaatgc gtcgaagata gccaccactg caggggcgtg 60

gcatgctgcc gtgcttccca cagggagatc aacacctgca cctccgcctc cttccgcggt 120

taccacgag 129

<210> SEQ ID NO 241
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 241

ggtgcgatcc agccacagaa agattggttt actcgataat tgaacggtag actttgtgca 60

ggtttagatt gtgtacatgc tgatcagtat tgtctacacc attttcaatc ttgtttagtt 120

ctatggtaat ttatgtaaca aattcagcga tgttggggaa attggtcaca tcagctttgt 180

gcctatatat ttcaagtaaa tcaggggatc cattaatact gcttttaaaa taattggggc 240

aaagttgtgg gatgactgct tcagcggaat acgtgctttt catagtgctg tatgacattt 300

tgttgaatat gaattttctt tgtgatacag ttgcgcgaaa aaaaaaaaa 349

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<210> SEQ ID NO 242
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 242

ggtgcgatcc atgccaagag ggtgaccatc atgcccaagg acattcagct cgctcgccgc 60

atccgtggag agagggcata aacagtcagt cagatccaat ggtgtgtttt cacaccacca 120

tatgtttctt ttactaaatt tgttaggtcc cttcggtggg tcttttcttt cccccgattt 180

tagtattttg ttgttcttct gagtttcatc attgcaagta caagatgcag aattgatggt 240

tattgggact tggagactgg ttattgctat gtagagtatt tatattagac aggtttcact 300

tgaagatata aaattg 316

<210> SEQ ID NO 243
<211> LENGTH: 188
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 243

ggtgcgatcc tcatgtgtta taaccgaagt ttgcgggatt cagatggtca gtatcttaaa 60

tgtccaactt tcggtacgaa tggggtgcgt tctgaaacgt gccacgaaag aggtgttcag 120

gatctgtctg aggcatcttt ccggtatttt ccacttccat ggtatgagaa actttcgtct 180

tgttgcag 188

<210> SEQ ID NO 244
<211> LENGTH: 170
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 244

aggagacaca actttacgaa aaagttcaat ctggagtctt ctaagttttt cagactctct 60

aaatatgaaa agcgccgagt ttctcctata ctggactcgt taaaatttta cagtaaagga 120

cctgttctat tacaaacagg aacggaccgc tcctccttag ggatcgcacc 170

<210> SEQ ID NO 245
<211> LENGTH: 164
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 245

ggtgcgatcc agcaagagaa cgaaaaagat atgaagaatc tatgaaatat ttgtacatca 60

ctgtattcat atgagggcct ttttttacaa tgcggtaggg ttgtttggag aattagaacc 120

tgattaaaat gtagatggat tcaagctttt agtgaaatga ggct 164

<210> SEQ ID NO 246
<211> LENGTH: 187
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 246

ctcaacataa agtcatagca tagcaccaca ccacagtcgt catcatttgt tttgttcacc 60

accgaagggg ctctttacag cgtccttgaa gccctgtata gcacccttcg ccttgtcccc 120

cgcctgttgg aagaaagagc cagtttgttc tttcccctct tgggcttttc ccgtgatgga 180

-continued

tcgcacc 187

<210> SEQ ID NO 247
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 247

ggtgcgatcc catgggatag ttgcaaaaca cacaaatttg ttgtgaaaga agagagacac 60

gcacagacaa ccatatgatc ttttttttt ttttttttt ttttttttt ttttttttt 120

tcgggaccaa atatttttca atacaacgcc atgtgacatt tttgtgcttc ttgtttttga 180

tacatacatt ccaaaaactg aacactcgat ggatacggtg atgatgcagc tacagccatt 240

gcattacaga tgttattaaa ttaaatcaat ttattatgtc atcacaccaa cccaaacaat 300

agcgctatta tgtcattaga atggttgcag ttacaagatc tgcaaacaga tcaatgaatc 360

atcatgcccc tctatatctc ttgtcaaaca tcaagataaa cctaatttta ggactggact 420

tcctcaatca tatcacaatg gcaaactcag cctcatgtcc tggatcgcac c 471

<210> SEQ ID NO 248
<211> LENGTH: 265
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 248

ggtgcgatcc tggactggcc atatgtgaag ataacaaaaa tggcgacgat gagttcaaat 60

atgcatagaa taagcgttct gtaattggaa cggccatagg agttggcacc tgttagatgt 120

gctggcaggc gtacatgtaa cggtggtaca tgcggtggca ggagtacacc gcaggtgtat 180

tgtaagagta gttggaacga tatatatgcc ttaacataaa atgtttaaga cttaatgcta 240

acattaattc aacattaatt catag 265

<210> SEQ ID NO 249
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 249

ggtgcgatcc catgggatag ttgcaaaaca cacaaatttg ttgtgaaaga agagagacac 60

gcacagacaa ccatatgatc ttttttttt ttttttttt ttttttttt ttttttttt 120

ttttttttt ttttttttt ttttgtttt ttttttttg tgaagtgaca aaatctaaac 180

caaagattaa aaggctttgg cttcagatac tatagaagaa tgagtctcaa agtggacagc 240

atacttgcgt tccgagcctc atttcactaa aagcttgaat ccatctacat tttaatcagg 300

ttctaattct ccaaacaacc ctaccgcatt gtaaaaaaag gccctcatat gaatacagtg 360

atgtacaaat atttcataga ttctcatatc tttttcgttc tcttgctgga tcgcacc 417

<210> SEQ ID NO 250
<211> LENGTH: 167
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 250

ggtgcgatcc caaccaggtg tccatgcaat atatggtgag catcaagttt gaggtggttg 60

attgaaagtt acaaattggt gacatctgaa gtctcattca gttatgtttt tgtatataaa 120

aaccataacc aattttgtat ataagatcca taatcaattt tggccaa 167

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<210> SEQ ID NO 251
<211> LENGTH: 236
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 251

gttttcaaga agagcctgac ggtttcctcg gcgggatgac ggaaacagga agcggccggc 60

cggttccgga ccctccgcag gcggagcata gcattttgcc ggaaccaccg catgtcctgc 120

acccaacatc cgcgtctgac cagcggaggc acatgcaccc aaccctcccg gttccattgc 180

acctcgggca gcgcggccac ccgccggcca tcggcttatc catcatggat cgcacc 236

<210> SEQ ID NO 252
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 252

tgggcgaatc atatggcttg cattttcatt gtaacatgta tacgttaagg attatcataa 60

tgcctccaaa accttgtatc ttcgtccttg ccacaataca tccaggataa ctaatggaag 120

cttgacatgt cttcaccagt aataatatat caactataat acatgccatt cttttatcag 180

ttttgaacaa aataatcgat ttgcattctt gacaaagaac ctcgcgcata aaaacaaata 240

aattctcata atgcctccca aaccttgtag tctgggccct cagtcgccac aatccattta 300

agaggaattt gggggttgat agtgcccagg tccaatcttc atgaaaattc gttcatcaat 360

ctttgctgca tacacatctc tctctgcttt cactatctgg gatcgcacc 409

<210> SEQ ID NO 253
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 253

ccactataat gaacattgat attacaaata taatatacat taatattaca attcaaatca 60

ttgacaatga gcaggcacta cttgcagtgc tttggaattc agacttctga tttgcaatta 120

attcttgtag acgcttttct gggagggcag gttttccgct tcagagaaaa ccacgtacaa 180

aacgatatta aataaaaata gacacataca aaaaatactt catttttgc tctttccatt 240

tggtttcttc ctctatctcc attttggagg gcttaaatga cttcaaattt aaaagtcaac 300

aacagagtgc agcacattct attagctttg ctgtaaatat ctgattggat cgcacc 356

<210> SEQ ID NO 254
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 254

ggtgcgatcc gcattaagag aagcatacaa gaaaaagaag tacctgcctc ttgatttgcg 60

tcccaagaag actcgtgcta tcaggcgacg ccttaccaag catcaggcat cattgaagac 120

tgagagacag aaaaagaaag agatgtattt tccaatgaga aagtatgcag ccaaggtgta 180

aagcacagga tttgagcttt catgcaattt ttttgttact cgcgggatga tattgcctat 240

tatatttccg tccaagtttt tggcaaattc ctatttgcat cagaattcaa gttatgatag 300

gtgttctttc gtttttgagc agttgatatt gtttatcttt tatttctatt attaatcttc 360

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taagttggat cgcac 375

<210> SEQ ID NO 255
<211> LENGTH: 189
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 255

aaacagacaa atatagaaat atgcatacat aagtccctgc agaattgttt tccgcaatga 60

attctggttt atggcaacat tacctactta gtactaaccc taagattatt ttcagctctg 120

ataagtggca tacgtgtatc aatcttgcat gagtctatcc ctgttttaat cttttgttgg 180

gatcgcacc 189

<210> SEQ ID NO 256
<211> LENGTH: 105
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 256

gtggaagctt cattgtaaaa cactactggt tttgagagaa caaaatatat acgctagccg 60

agtggattat aacaaaatat aggctttatt ctattggatc gcacc 105

<210> SEQ ID NO 257
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 257

ggtgcgatcc catacattaa catagccatc acagccccca gtggcaaaag taccatagct 60

gcaaaaacat tataaaacta acattcctac aaggaaataa aatacaacta aaaaagcaag 120

caataggcat taggggaggg agaagctaaa actattaagc aacttacatg ggatgaaagg 180

caattgcgtt tactggataa acagtatctc tgccagcctc tgacttgcga tgacatttaa 240

aggcatattt tttaagcttg accagcttca gatacatcat aatactccat agccatgcga 300

gcttccacag aactaagggg caaaacctgt tccatttgga tcgcatca 348

<210> SEQ ID NO 258
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 258

ggtgcgatcc aactgagaag ggtgtttggt ggaaagatga caccaagtgg gttctctatt 60

ctccagagga tgcaagaaaa attctgagag caaagaagaa tggggactca aatattacgt 120

tgggttctgt taaatctgcc aagtaccctt caggaaagct ttatgccata gacctggtgg 180

ccatgaagca aaccaatgta aacactggct tctccagaga tatcaaaatc atcaattctt 240

gccctactga tgatcaggaa gatgtagagt ctgatgaaga agatgaatta ttcacattct 300

ctcgtcctgt caaagttgaa gtgattaacc agagcaggaa acctgataag attgtcaaga 360

tggttccttc tgtcactgta gaccttgaga aattgacttc tcaatacctc ctggaggatg 420

agtgcaattt ggttctaaag cttcccaggg ctgcagctgc ccaatcggat cgcacc 476

<210> SEQ ID NO 259
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 259

ggtgcgatcc agctaatcaa acttaatgga gagcccttcc caggaagagt aaatggtagt 60

cacttgaagc cctacacggg tgggctggcg gtctgactaa ctgaccaaaa catagtcttc 120

gcgacccaac aagccagaca gaggtgtggg actataagca caagtactag aagctagcat 180

caaagtagag aattaagtta gatacagatg attcagaagc agaaatggag cagatccaga 240

ccacggtagc atggtgagtt acgaaccttc acgccacacc aacgcaattg gttaagactt 300

cgcactagga tcgcacc 317

<210> SEQ ID NO 260
<211> LENGTH: 283
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 260

ggtgcatcca tagttccttt tgctaagcga ctactctatc tcttttgaca tttctccaaa 60

tattgggtct ttcagttcct tcaaatgcta gaatcatatc aacatgggat ttagtgaggc 120

cgcaatacta accagggcat taaaataata catttcattg atcctattcc caaaacattt 180

cccgctatcg tacgttgact cagcatattt agagcaattc ttcttacaaa ccttaagaag 240

gttgttcatg atagtctttc cgtctgcaat attggatcgc acc 283

<210> SEQ ID NO 261
<211> LENGTH: 299
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 261

ggtgcgatcc cacccaagag ttaaattcac ttctccgcct ttctgaggaa gagcactctt 60

tggatgatat gaaaagtggt ccactcttaa aaaccgtatt cggaaccctg ttccgcggac 120

ggtcgtatgg cgtaaccggc gcagacattt tatctcctca cacaatatca acattcaagt 180

ccccgctgtt ccccgttgcc tttctctgct cccgaccgtt aaacaagaac gaccacaaga 240

atgaacaaca ccgcaaccga aacctgaccc tccacgttgt cttcggttcg gatcgcacc 299

<210> SEQ ID NO 262
<211> LENGTH: 352
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 262

gcggacgcct ggcaaaaaca gagggtatgc tcaagcctta cagaaattga aaaataagag 60

aacgtatgac catcaatctc aatctcaaga aaagaagttg caatacgact ccaacacttt 120

tgaaagttgg aggtttgctc tttctagcgt tgcagacatg gttggttttg agctggaagc 180

gtgtaacggg cactttacag ttgcgggaat tggagattga ggacccccctc tcaaacgtcg 240

atagggaggc taagcatcta tagaggattg tgattggtcc ttttccgcta catggaaaga 300

aagtcaaact cagaaaatta ccagaagaat tctgtcgtct tctcgcagcc gt 352

<210> SEQ ID NO 263
<211> LENGTH: 221
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 263

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gacgttgtaa aacgacggcc agtgtaaaga gcagccccga tgcgccgaag ctcgcgaggg 60

aaaagctgca gaagatggga ccgatgacca agaatgagat catcatgagc ggcacgctac 120

tggtcacggt gggtctttgg atatttgggg gaatgctgaa cgtggatgct gttactgcag 180

cgatccttgg tttgtctgtc ctactctgca caggcgtccg c 221

<210> SEQ ID NO 264
<211> LENGTH: 365
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 264

tacggctgcg agaagacgac agaagcagaa cctgccaata taggatcaat tgaatgttgt 60

gggattgctg catgcccacc tttcccagtt attactgcct tgaagaaccc acagccagcg 120

agtaagggcc cgggtttcga accaatcaca gatgtaggat aatcgcttga aacatgcata 180

gcgaatatgc cttccacatt ttccagtgct ccctcctcta tcattctttt tgatcctgca 240

cctgattcct ctgcaggctg gaagagtaat atgacagttc cctgtaacaa atgctgacgt 300

tgttgcaaaa tctttgcacc accaagaagc atggtaacat gtgcatcatg tccacaggcg 360

tccgc 365

<210> SEQ ID NO 265
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 265

tacggctgcg agaagacgac agaaaagagg caaaccgagc tcgacacctc cactcagagc 60

atttgcaaaa atccacaaca aatctggagc caaggtcttt ccctcattga aaacatttat 120

cggacacatc aatgtctgta gtctttccca tggtccatcc agagtaatca cgggaagaac 180

aatgcacttc agttcagaat ttttgatgac agctatcagc tcctgatcct ttgaaccagg 240

tatataataa tcttgacctg actcctgttt caacagtgta gaggttctgt caacctcaag 300

caatgaatcg gcagaacttc catttgctgt tttgtcaata caggcattgt ttttaccaag 360

actgtgacgc atcttctgtc cttgtctata cagtgcagtt tgttcaagca tagacttatg 420

tgctagaaca tgtcttcctt ttaaattgta agagaaatgt aggggttgac tgcttttact 480

gaggcgtccg c 491

<210> SEQ ID NO 266
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 266

acggctgcag aagacgacag aaccctggct gactacaaca ttcaaaagga gtctaccctg 60

catctggtgc tccgtctaag aggaggcatg cagatttttg ttaaaaccct tacaggcaaa 120

acaattactc tggaagtgga aagctcggac actattgaca atgtaaaagc taagatccag 180

gacaaggagg gaatcccacc tgaccagcag aggttgatct ttgccggaaa gcagctagaa 240

gatggtcgta ctctggccga ttacaacatt cagaaggagt cgacccttca cctggtgctc 300

cgtctccgtg gtggctttta ggttggctgt tgtgtgtcaa tgtagtctgg tgatgttcag 360

tggttttcct gcttaatcct ttttatgtat gcatgtgttt gttgtgtttg tgttttgtct 420

ctatgttttt tctacttggt ttgtcggtcg gttgaagccc ggctggtgtc ctggtaggcg 480

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tccgc 485

<210> SEQ ID NO 267
<211> LENGTH: 494
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 267

gcggacgcct ggacaaacac agaaggcgaa gtaaaagcca gtcttacttt tcatgtaaat 60

actatcaaac tgcatggccg ttccgctggt tggcaatacc acacctgcgc cggtagtgcc 120

aatgaacact gcaccggcag ctctttcaga agttgcagag gacttaccat tttaattttc 180

acggcatccc gtcaaacggc gggatgcttt taatttttta atcaaaaaaa atattaatta 240

tggcacacaa tattgttttc aacgaacaga caggcaaaca cagtttcttt agtgtaaaag 300

aaaaagcatg gcatggtttg gggcaaattg tacaggacta tcccaacagt aaagaagcat 360

tgcaatttgc agggcttgat tttgaagttt gcaaaaggcc caatattcac aggcttgata 420

atggtaatga gattatttct accagttcat tctatactta ccgtcctgat accaacgcca 480

tattaggcgt ccgc 494

<210> SEQ ID NO 268
<211> LENGTH: 469
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 268

gcggacgcct gaacatagga gcattcttaa gcatatcagg tataaccata aacctgactt 60

tgctgccccg aataaagaca tgctccaatt gggatacttt tccatccttg gcagtgtaag 120

tgatgccctc gagctggcaa ttccagttat cttcgcattc gatcatgcta cccctgtaca 180

gctcgccact tttgagttca actgtcacaa catgcccggc tgcttcatgg agcaacttca 240

caggaatccc caaacttctg ctcatttttt tgtcactgct caaaaaccct aaaccccaga 300

taaaaccctc ggttctgtgc cttttatccc cgggtggctt attgttgcag tagttggcaa 360

cggctagact tactcacatt ttgatttcaa tctttctaag tttgcccttt tgggttttcc 420

tcacagtaga tcctatttta tgtattttct cgtcttctcg gcagccgta 469

<210> SEQ ID NO 269
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 269

gcggacgcct gcaggaatcg gccgatttgc agttcgaggc ataagcgcat cgaggtcgcg 60

ttcgatgtag caattaagcg cgcatgaacc gccgctaagc aagccagtcc caatcaaagc 120

acatgcaaag cggatgcaat caaatcttcc gttgtaagca agcacaaatc caactgcaca 180

tgagatcacc accatgaatg caattcgagt gcgagctaaa tcccaaaacg ctgcgagtgt 240

cccctgaagg cgattcgtat gtaatatttg accgctgctc aacacaagca gtactccaaa 300

caccagtgct tccgccgtca attctgtcgt cttctcgcag ccgta 345

<210> SEQ ID NO 270
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 270

ctgcgagaag acgacagaac acagacacaa aatttggaaa ctacagaaaa gaccatgtca 60

tgaaatcttc ataattgggc ttcagatgca gaggggtcg gttttggatt aagcaatggc 120

tgaagtgctt tgacaacaat actcatgtta ggacgaaaat ctgcttcata ctgcacacac 180

aatgccgcaa cagcagccat ctttgcaaca gcctttggag gatattcact cttcaacttg 240

ggatcaacac actgctttac tttgtcttca ctcaatcttg gagttgccca agtaacaagg 300

ctttgttgtc ccctaggcat tgtatggtcc acaggcgtcc gc 342

<210> SEQ ID NO 271
<211> LENGTH: 313
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 271

tacggctgcg agaagacgac agaaagagac aggcttggac ttcgtggcct tcttccacca 60

cgcattattt cttttcagca gcaatgtgat cgtttcatgg tttcttttag atccctggag 120

cataacactc gagatggttc agctgactta acagctctgg caaaatggcg tattcttaac 180

agattgcatg acagaaatga aacactatac tacaaggttc ttatagatca cattgaagag 240

tttgctccaa taatctacac tccaactgta ggattggttt gtcagaatta tggtgggctg 300

ttcaggcgtc cgc 313

<210> SEQ ID NO 272
<211> LENGTH: 277
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 272

gcggacgcct caatagttat ggaagggcag ctgcactact tcagcatgag tggaggccta 60

aaagttttgt taatctttct ggtgaggtgg acaccaaagc ccttcacaac agtgcaaagg 120

tggggctatc tctggttttg aagccttgaa ggatatgcac tatttggtac agatttaagc 180

gaaggtctgt gccaaatttt tattggaatt tttgagtttt tcctttcaga ataattattt 240

caatgcctgt gttttctgtc gtcttctcgc agccgta 277

<210> SEQ ID NO 273
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 273

gcggacgcct tttgcccaat taacatccct gcatctgcgc attaaaaatt gattgcagac 60

ctgaggttta agtggaagct tcttccacca tctctcccct gtttaaggaa gacccgaaac 120

cctagccact gtctcctctg tgacttaaaa ttccagttca ccaaccttaa ctctgcgtcc 180

gttaaaattc tgggcaaact gcactgccaa ttggtcatca tatcctctga atttggcaaa 240

gaaaacatag gtcattctgt cgtcttctcg cagccgta 278

<210> SEQ ID NO 274
<211> LENGTH: 180
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 274

gcggacgcct cgtcaatcca tggttgtaaa catgccttca aaactgtttc cttatgtcgc 60

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acaatgtcta catgttcctt gagcgatttt tcctgctgca ttgcgagcct ctgtgtaagt 120

cccactatct gcgctgtccc ttttacttca taatacttct gtcgtcttct cgcagccgta 180

<210> SEQ ID NO 275
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 275

tacggctgcg agaagacgac agaaaaaact gtatacgagt aggcagcgag tcctggcagt 60

atgggagatt gaactccaat tacatttagt tacaagtagc atcaacagtg actgagccaa 120

gagctctaca cagaaaaata aaataaaaac tgtatatatt tacaggagaa accccaatgg 180

cctcagggcc tgaataaatc aatcgcagcg gtggtcgatg tggccttttc agggctgcaa 240

atcttgcaag gggaagccat catccttgtt ccgtatcctt tttgagggat agcgagccac 300

gcagccaaga tttgaagcga ttgaatactt tggggtgtcg agaacgcacc agaacaatgc 360

cactcgagaa atactactgt gattactgtg acaaacaatt ccaggatact ccctccgcta 420

gaaagcgaca tctacaaggc gtccgc 446

<210> SEQ ID NO 276
<211> LENGTH: 425
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 276

gcggacgcct gtaccgtatt ggaattctaa acccttcctt ggtatagggt tttcgccacc 60

cttgcgttca tttggttttg tattacgtcc gattcctccg tctgcgagct ctctgcaact 120

tggcaatttc attgtgattt tatcctatga tgcttcgtat ttgtttgaag ctcgtcctcc 180

tagttctctg tgataccagt tggtagtctg caagtttcga tgtgggttct tttagctggt 240

ctggggtttt gttgctctga gtatgttgag ctgcatgctc gtggcggtct tcacggctcc 300

atttgttcgg aatctgttgt ggaagtgtct cggtcatctg tggaactgtg gaaacctggt 360

aagatttgtt tatctgcttg tgtctaaact gttcttgagt tttctgtcgt cttctcgcag 420

ccgta 425

<210> SEQ ID NO 277
<211> LENGTH: 295
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 277

gcggacgcct gctgttgaag aaggatgaag tcattgtctg cggccctgtt cagcatgatt 60

tcggcattct taatctggtc aaccagtcag aaggtggcgc tgaaggtgac gaagaggcaa 120

cctgggtagc tgcactggaa actcaagctg caaggggcac cgaccctcag acttcgcgcg 180

attaacttct ccctctggct aagtcgatgc caaggtcctt gttctgggtt cttctctctg 240

tttcgcatgt tgttcttctc tctgtttcat ttgtttttct tctgtcgtct ctcgc 295

<210> SEQ ID NO 278
<211> LENGTH: 196
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 278

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gcggacgcct gcacatacaa agaacgacaa aaacaaaagc ataaaatcca atagatgcaa 60

ctatatatca agtcagaaat gatataactc atcattatta caaagaacaa taagagtgga 120

accataataa tagtcgtcta ttattgataa ataaagaaga atacaaccat agttctgtcg 180

tcttctcgca gccgta 196

<210> SEQ ID NO 279
<211> LENGTH: 172
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 279

gcggacgcct gtataacatg caccaagaga cccaatcaaa gcacatgcaa tctgtatata 60

tagcagaata acagccaggg attgcactct atcgtaatcg cgaaaccacg cactaatatg 120

tgcccatgct gatgatgcac acagcatgtt ctgtcgtctt ctcgcagccg ta 172

<210> SEQ ID NO 280
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 280

gcggacgcct gaactgtata gagttgaaac ttgagggaag gcttgctgcc accaaagcct 60

ccctcctctt tccttggcgg ttcgtcacct cctttcgcgt cagagcccca attcccctcc 120

tgcgcacacc agcaaactgc atcgaatgtt ttttccacca ttctgtaaat tccctcggag 180

ttaccttggg gcagaagccg cattgaagag cattgaatgc tattcattat cccaccgtaa 240

actaccattg caacctgcct gtgtatcgac ccgctgtcct ctacgcgtgg ctggcacatg 300

gcgtcgttaa ttgcatgttg acacccgtat ccgggtgtgc ttgtgtgctc gtctgcatat 360

catgttttag gatctcatag aaggtggacc attctgtcgt cttct 405

<210> SEQ ID NO 281
<211> LENGTH: 412
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 281

gcggacgcct cttacaatgt ctcttaaaga ttggaaagat tgtcttgtct gcaaccataa 60

cttccgcgtg ctttcttatt aatgcaaccc actgtgatcc tttccgccat ttatcctttc 120

gaatggttgg agccattttt gggttgtacc gactagcttt tgggtctaca aagctgtcta 180

caaaactctt tggagatgac attacataat catatgtata gctgaagttg tacaaaggta 240

cacaactatc tgaaaccaaa atgaatctct cgttagctgg atcctcgagt gctttcctaa 300

gtagaatacg ctccgcttct atcatactgg cttctcccca aagtacctgt atgctatcac 360

taagctgcca gccgtaacaa aatgtacatt ctgtcgtctt ctcgcagccg ta 412

<210> SEQ ID NO 282
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 282

gcggacgcct tgctaggaga gctctacgcc attatttgaa cgattgagcc gaagtttcac 60

cgtttaaggc atttgtgtcc cagaggttat tggagattag cagcttggat ttggctgctt 120

cgctcagcgc cgtgattcag cttttgattg attctctcca gtttcataac ctgtaacgac 180

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aatggcaatg aagacctaca catttgcagt ggcagctgcg tacgctgtag tcctgatgtt 240

cgctctcttt ggcatcgcaa aggctgctga tgcaccgtct cccagccccg ttactggcgc 300

gggttccatg gacttcgttc cttctgtcgt cttctcgcag ccgta 345

<210> SEQ ID NO 283
<211> LENGTH: 218
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 283

gcggacgcct tatcagctgg gggcattcat aggtatggaa attcagatca acttcagtgg 60

acagtatgtg gatttaggcg acctgtgaca gttcacgata tctattcatt tctatccaga 120

gacagattcc catactcacc tccgtccttc ccatatattt tctggaaggc atcatgtcct 180

cccaaattta ctcattttgc ctggccgtcg ttttacaa 218

<210> SEQ ID NO 284
<211> LENGTH: 219
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 284

gcggacgcct gttgccacag aagaatgaat aatgcttcaa attttgagac ctcttcggag 60

gaaaatcctt gttcttactg cctaaccact catgatgatc tgcgtcacgc tgattatgag 120

ctgcaattta aattatttca gatgaaacat tcccatattg agcttgcaga caagttgcag 180

acccttcaat ttcagttctg tcgtcttctc gcagccgta 219

<210> SEQ ID NO 285
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 285

gacgttgtaa aacgacggcc aggattaagg ttcatgagct ccgcaacaag agcaaatcag 60

<210> SEQ ID NO 286
<211> LENGTH: 732
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 286

gcggacgcct ctaggagccg gcggaattcc tgtgagctcg aatttgccga gcaggttatt 60

gtccttcgtc cgcgctcgct caccttcata tacttgaatt agaaccccag gctgattatc 120

tgagtaagtt gagaaaatct gctccttctt ggttggaatg gtggtgttcc tcggtattaa 180

tactgtcatt acacctcccg ctgtctccaa ccccagactt aatggcgtga catctagcaa 240

cagcaggtcc tgcaccttct cgttgccttc gccgctgaga atggcagcct gcacagctgc 300

accatatgcc acggcttcgt ctgggttaat gctcttacaa agctctttgc cattgaagaa 360

atcttggagc aattgttgta ctttggggat acgagtcgaa cccccgacca agacgacatc 420

atctatttgg ctcttgtcca tcttagcatc ttcgcataca tttctccaca ggctccatac 480

ttctcctgaa aagatccatg ttgagttcct cgaagcgagc tcgcgtaatt gtggcgtaaa 540

aatcaattcc ttcatataga gaatcaatct caatcgttgt ctgtgtagta gaagacagcg 600

ttctttttgc cctctcacat gctgttctca gcctgcgaag agctctggca ttcccgctga 660

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tgtcttttct gtgctttctt ttgaattcct gcacaaagtg attcaccatt ctgtcgtctt 720

ctcgcagccg ta 732

<210> SEQ ID NO 287
<211> LENGTH: 100
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 287

tagccatcgc catttctata atcttaggat ccttgctgaa cgataagccc ataaaattga 60

tgcactgcct cgctatccct ggccgtcgtt ttacaacgtc 100

<210> SEQ ID NO 288
<211> LENGTH: 347
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 288

gacgttgtaa aacgacggcc aggaaattac agctacctct aactggtttg acggcgttgc 60

atcttatgag ccgcaagggt tcgaatcctc tgcgggccag atctgcgatg gaaccctggg 120

cgagtgcaat gatgatgaag aagagtttgc gatggattct gaagcgcacg ggaggcttct 180

gaggaggatc cgttactata tcagctacgg agcattggct gctaatcgcg ttccttgccg 240

acctcggtct gggaggtctt attacactcg gaattgttac ggcgcaacag gccccgtcag 300

accttaccac agaagctgca ctgctatcac tcgttgcagg cgtccgc 347

<210> SEQ ID NO 289
<211> LENGTH: 106
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 289

gcggacgcct gggaagcaat ggatgggtgg ctagacgcca tccgtcttgt gtatactatt 60

tttgcacgcg gaaagagtga tgtcctggcc gtcgttttac aacgtc 106

<210> SEQ ID NO 290
<211> LENGTH: 307
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 290

gacgttgtaa aacgacggcc agattcaaaa gaaaaaatcc tcacttcttg gctccgtttg 60

cgctcccgcc gaagctcctc tgcaacccct ctgcagcgta cactgcatcc cgctcgcggt 120

gctggctcac ctcgcaggtc cgctgacggt aaatggtttc caataaagct atttgtcctc 180

tacccaaaat ccatctagca ttcgttgtgg attgacattc tgccatttct ctgcttttct 240

ggttgatatg caaagattga aagcccaatt gcaagcagtg gtcgtggatt cactataagg 300

cgtccgc 307

<210> SEQ ID NO 291
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 291

gacgttgtaa aacgacggcc aggaataaaa caaagcatca ctgcaaaatt tcaaacgtgg 60

taataacggc tagccagctc gacgtgaagg cagtgggggc cttgaggttg ccttttggcg 120

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ttcaaaattg gctagactac cataacataa atattgattt ctcagtgaca tcactggttt 180

ggagtcatcc acagcctgtg caccagtacg gcaattgcct tttacatgaa gccatccttt 240

cacttttact tttgagattc tcagaactga ggggctaggc gtccgc 286

<210> SEQ ID NO 292
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 292

gacgttgtaa aacgacggcc agcaccttcc tagtcccctg ttccattctc ctgaaatagg 60

agcagtttga cccagtccag ttttcagaat tgagaatatg aaacaaagaa cctaagcata 120

tgagagaaca tacaaagact ttgtataaac tacttttcac aggatctcaa cagccctctg 180

ctgagatcca tttgatacaa ggccccttgc atctccaccc tctcccttat cacctccact 240

agaaagatga tggaaagcag acacatggaa atgttgctgc aggcgtccgc 290

<210> SEQ ID NO 293
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 293

gacgttgtaa aacgacggcc agttaggttg tatattgatt gatgactctt tgactccatt 60

tatgaaaaca tctttgttct cgagatttaa tcagtattaa gctttcagag tgaagttcag 120

tttgatctgc ataaacctga tccaccatat ctacatcaca tctaaaatta ctaaaatgtg 180

aggagatgga atttgtttct tgagaatccc tattcctcat cgacactgtt tactggatca 240

gatccaatca aactcttgag aagtaatctc tggaaagaaa ttaaaaagtc tttacctgaa 300

ttatctcgat atcagaagca gaaattatga tacatagact tcttaataat gaagagtcat 360

tttgccaacg ttgtctttgc caccccacca atccccatga tcccaaagat ctgaggtttc 420

catctctatg tggctgtgat aacactggat ttttcaaaaa tcttctactt tcgcatccaa 480

acctttttgg gatattt 497

<210> SEQ ID NO 294
<211> LENGTH: 238
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 294

gacgttgtaa aacgacggcc aggggggatgg gagatacaga aagattccgg ataaaaggga 60

gcaatgaacg gctggttaaa gcgtagtcca ccacactagc cccacctcca tgaggcctac 120

acgtgaagaa gcaggattct gggaagcgcg agaggccgtt caagattatc agctcatgtg 180

attcgcccaa ctgcaaaaga tgtctaccgt aggctgtgat ggggcccaag gcgtccgc 238

<210> SEQ ID NO 295
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 295

gcggacgcct atcagatggg tgagttgacc gacatttatc gtccgataaa tgtttgaggc 60

tgatgtcatg gcaatccacg tgtctgcacc atatttcatc ggagcccctc gtcggaatat 120

-continued

tccatcgccg gagagctggc gcgataggtt tcaggcggcc ggtttctggt ttgcagctgt 180

ggcttcccgc gcgccttaac tgttggcccg cgcgcacagg ggaaattaca aatttcaaca 240

tatccaatac catcatataa cccaacaaca ctagcaacag atcctgttct gtgccatcgt 300

ccaactcttg a 311

<210> SEQ ID NO 296
<211> LENGTH: 202
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 296

gcggacgcct taattcgact acaaagatac tgaagccaat gatgacaggt tgtgccactt 60

tcccagctga taaagacagc tctgaaattg atagagccag aactccagct gcaatgctcc 120

ccagagcctg gttgaagcgc ttgctaaagg tggcacttta tagaccgacc caaaacctcc 180

ctggccgtcg ttttacaacg tc 202

<210> SEQ ID NO 297
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 297

gcggacgcct actggaaacc cggtccaccg aaggctgaaa ttgtcctgct ttgtataccg 60

aatggcagga aggttgtcga gcatcaggtt cacctggtaa agattatcga tcctatgctt 120

caataccttc agctgctctg ccccaaggac agtagtattg cacaggtaaa tttcagattc 180

attgacattc atccggaagc gatatggtga gttctcgatc ctgtccccca tgaggagctc 240

cccaagattt tctgccatgt ccttcacacc atccaagggc ttgcagaagg gcaggctgta 300

atagctgtag ggaagctctg tctcgactga ggtaagggaa ttgacgttca cccataaatc 360

tgacccctgg gagaatatga tgtgaggaat acagtgccca gtaaatataa ctccgcatta 420

tacgtttgtg tgtgccttcc ccaatattgc cccaacataa tcaaaaccca caatcccaaa 480

tcctggaccg tcgtttttac aactgtc 507

<210> SEQ ID NO 298
<211> LENGTH: 522
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 298

gcggacgcct tgtcaggacc aaatgtgtaa gaaacacctc tgtcattcga gccccatcct 60

tgaattgcat tgcaggggtc tgaccaaaga agatcacata acaaccctgt atctggcaca 120

tctgtaggtc gaggtatatt ctttatttgt tccaaattgg tcagttcagg cgaaagacca 180

ccatgcatgc ataggatctt ttcatctata agtgcagcaa caggcaggca gttgaaacag 240

tctgtaaaaa gtttccatag tcttacattg aatctgcgct tgcactcatc atagaaacca 300

tatatgcgat ttattgaggc acattcatga tttcccctca gaaggaaaaa gttctctggg 360

tatttaattt tgtaagcaag gaggaggcat attgtctcta ggctttgttt gccccggtcc 420

acataatctc ccaagaaata agtaatttga ttctggtggg aagccaccat attcaaaaag 480

ccttagacag atcagaatac cggcctgtcg ttttacaacg tc 522

<210> SEQ ID NO 299
<211> LENGTH: 410

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<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 299

gacgttgtaa aacgacggcc aggagacggg aatacctatt tttgggagga ttattgggct 60

cgggaatcag catattgatg tggctgcaac tcgcatcctc gatctttggt ggttcttcgg 120

cgatttacac atttgagatc tacttcggtc tgctagtttt ccttgggtat attatatttg 180

acacacagat gatcatcgag aaagcggacc atggagacta tgattattta aaacattcac 240

tggacctctt tattgacttc gttgctgtat ttgttcgcct gatggtcata atggcaaaga 300

atgcagacag taaatccagg gaagggaaaa agaagagaag ggcttgaact atgtgagata 360

caaaaatatc gagaatagaa gggcttgaac tagggcttga aagcgtccgc 410

<210> SEQ ID NO 300
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 300

gcggacgcct atcagacaag ggttgttgac cgaactttat cctctgaaaa gtgcttgaag 60

ctgatgtcat ggcaatccac gtgtctgcac catatttcat cggagcccct cacacggaaa 120

caaccttaag ccaaaaggtg gtgcgatgac ttaccggccg tttatggttt gcttcggtgg 180

ttttctgttg ggtggtttcc cgcgcgcgtt aactgctggc cgtcgtttta caacgtc 237

<210> SEQ ID NO 301
<211> LENGTH: 625
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 301

gacgttgtaa aacgacggcc aagaggggga aactcccaaa acacttttcc atttttcttc 60

ttttattaaa cttcaaagta ttttccaaca gagttacaag gggccaacca tgtccaaatc 120

catgcattta ccaagtacaa agaatggtag tccttggctt gacctatcgc actagccaaa 180

agtgccaagt ccacaactag ggtgtgccca acctaaggtt gacaccttgc ctagaaaaaa 240

ccccaaactt ggcaccacaa ataacacaga aacacaactc ttgacctctg ccagaaacca 300

ggctctcttg ggaaagccac acctctctct gtgatatgtc ttatctccaa tttccctttt 360

tgtgatgcac tcccttgctt gtggttctgc gatatcacac aaacttacat ttctgcgatt 420

tttgtttctt gcttctccaa atcatgcgat cttatttttа acccttgaga cccttcacac 480

tttccatcca tgacgtcact tcatcgtttt agccaattcg tcatttgggc atgttgggcg 540

ttgggtctac ccgtattccg gtcgtacagg ccaaattgac cattttggtc caggtgggtg 600

cacccattcc tggagggcgt tcggc 625

<210> SEQ ID NO 302
<211> LENGTH: 629
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 302

gcggacgcct ccacagagct cacacataca atatactatg atgcctccag aactatggca 60

ctctgtatgc cgcttcaata tggattagcc cacactgcgc catccaatta ggcgaatcaa 120

ccttatagca ccatccacaa cctccagcgc tctcttttтc acgctagatt ggccaactac 180

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aggctttaca acactactca tatacaactc aactcggctc ctctgctcac cactaaatca 240

cacaggctcc aatcgctaga cagagccact acacaggcac taatagccac tacacaggca 300

ctaatcttgg cgtcctccac caggttccaa caacaacccc aaattgcata tgcactccac 360

agtgagcacc aactaggtcc acacaatagg ccacaccaac aacactccaa ggaccctaga 420

tcctgcctca cccagacacc actaggcctt cctcacagct cacctaagtg agccaacaac 480

tggctgggca cacagctccc aactatatga gcacacagcc caactacagc tccaccacac 540

gcacagctac acgcacaatg ccttctcaag ttcacagcca caccataacg cagcacagtt 600

cttacaaaca tatctctcca ggcgtccgc 629

<210> SEQ ID NO 303
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 303

gacgttgtaa aacgacggcc aggataatgg acacgagaaa cctttggatg tgcctctaaa 60

gtgcgggcaa tccttaaagc tgttgaattt tgttgctgta cacgaaggtg cagggtcttt 120

atgccacgaa gaatcaagta cgctgcattt ggacttaata cacctcccaa gacattgtgc 180

aaagcacgta ctgtgccaat aaccttgttt gaaccactca aactgcctgc aagaacatca 240

ttatgacctg caatatattt agttaccgaa tgcaatacaa tatctgcgcc gagtgctaac 300

gctttctggt taacaggcgt ccgc 324

<210> SEQ ID NO 304
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 304

gacgttgtaa aacgacggcc agtcattatt gacaataatc ctttcagctt tttactgcaa 60

cctttaaacg gtataccttg cgtttctttc actggagcac actcagatga taatcagctt 120

ttacaggtgc tcttacctct gttgaagcat cttgccactc aggaggacgt gcgccctgtg 180

ttgtatgaaa gattttacat gcccgcatgg tttgaaaagc gtggcattcc agcatctgag 240

tggcccttgt gacttggttt tgattttgga tactctttgt cattttgggt caaggtaaag 300

gtgtacgtat ccaagtgatg caagcgtccg c 331

<210> SEQ ID NO 305
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 305

gcggacgcct gatagcacga gtcttcttgg gacgcaaatc aagaggcagg tacttctttt 60

tcttgtatgc ttctcttaat gcggatcgct ggctctgaga aatcacagtc agaacctgag 120

ctattgatag cctcacgacc ttgattttag agagtttgtt gggcgctcct ccagtgacct 180

ttgcaactct gagcaaggca agctcagcct tgagctcctt gacctggctt aacagctcgg 240

atttgccctt gtggcggact caaggacctt taacctgggc gttcgt 286

<210> SEQ ID NO 306
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<400> SEQUENCE: 306

gcggacgcct ggtgtcgctg ggccagttca agtattttag caacagtgtt cacacttatt 60

ccctgtgata ttcttgactc acacaaccac cttaactgac gcagaccata tcgatctgct 120

gctgtaagca aatgttcgat cattgtctca ggtgtcaaaa agcaagggga tggatcagaa 180

agctcttcta aatctgcatg ctcctctaaa tctggaaggg tatctttgta aataaagtgt 240

aacatagcct taaacacctc tggccgtcgt t 271

<210> SEQ ID NO 307
<211> LENGTH: 283
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 307

gacgttgtaa aacgacggcc agaggtgttt aaggctatgt tacactttat ttacaaagat 60

acccttccag atttaaagga gcatgcaaat ttaagaaaaa ctttcctgat tcaacccccc 120

gccttttggc accctgaaga tggttcaaca atttgctaac ggaaccaatt caaaagggcc 180

gcctccattt aaggtgttgt gttagtccag aatatcacaa ggaataagtg ttaacaccgg 240

tgccaaaata cctgaactgg accaacgaca ccaagcgttc gcc 283

<210> SEQ ID NO 308
<211> LENGTH: 259
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 308

gcggacgcct tgtaatccag ggccttgaat attgtaagag aagatcgaga aataatagtt 60

ttcttattat caggaatcac agcttgaaga aggcagacca tggactccca ctggcttcgt 120

gatattgagt ccccaacaaa cattagtcgt tttcccctca atctccacag caagtctctg 180

gcattgaatc tgcgaaagga acacccgagt ggcttccacc tccatttctc gtaatcagaa 240

tctggccgtc gtttaacaa 259

<210> SEQ ID NO 309
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 309

gacgttgtaa aacgacggcc agcagaagac cagtgcagta tgctgcagca tagtttgtaa 60

gccctacttc gagtccataa cgaggcaact ccctagaata agcagccgac ataacaacat 120

ctcccgcaag agttgcataa atgatctgtg ccaccacatc cttgttgctg aatctaacga 180

ccaatcggta tttgggtgtg ttgtacttgt tcttatcttg gttaatcagg cgtccgc 237

<210> SEQ ID NO 310
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 310

gacgttgtaa aacgacggcc agcatccatt gcagaaattt tgggggctat atttagcaac 60

agatatcaca gctgtaagtt caaagttgga cccttcttct tcgacatctt ttccagctgt 120

gcaataaact gaacactgtc cttttggata agcttcctca acatatttag aaagttcaac 180

-continued

atccaagaca ttgcggtact cctcaacata tatggatgca agttcatcat ctgcagctgg 240

tctcaccgct gtacaaactt gtttaacatg gttgacagtt gcaacttgag cagtccgtgg 300

atccaaataa tgagttccgt caagctcact gaactcagtc acaatcacct ggccactttg 360

attgggcatc tcgagggata tcatgtgaga cttgttgtgg atggggaaag cgtccgc 417

<210> SEQ ID NO 311
<211> LENGTH: 308
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 311

gcggacgcct gcataaacat cgctaccctg gggatgatta ataatagtac cagggttagg 60

attttcttca tcttgagcga tatcatcata cataaagacc acaatgtttt cctctttcaa 120

accgcctttc ctcagaattt ggtaggcatg gcagatatca gcctgatgcc tgtagttcca 180

ataaccggaa gaaccagcca acagaatagc ccactgagta ccgatcgtat cactatcatc 240

aacgatatga tcggtgggca ttttcagtac tgaatcccaa ccccttctgg ccgtcgtttt 300

acaacgtc 308

<210> SEQ ID NO 312
<211> LENGTH: 183
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 312

gcggacgcct agactgggca taccaactac cttcctcatg ccaggccatg ggccacctac 60

ctggtactta ggcataacac cttacttacg agcatgccag gctcagtcag ataggcatgc 120

atcccaccca cctagctatg acccaatcct tataaacact agatattctc cctggccgtc 180

gtt 183

<210> SEQ ID NO 313
<211> LENGTH: 255
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 313

gcggacgcct agacaatcat taactgaaga tctgtaagcc atgacaagac gaataaaacg 60

aagcacggcg caaccagcgt gaatattgac gccttaattt cattcaactg ggttgcggat 120

tctttattcc tcaacaagtg ttcgatagct tcacatacgc aaggcccctt ttactctcac 180

cttcatggtt taatgctgta accgtcgaag gttgatgaaa ggacttggat gatgatgttg 240

ccaaaaaaaa aaaaa 255

<210> SEQ ID NO 314
<211> LENGTH: 184
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 314

gcggacgcct gctcaacacc tgttatagtc atttcttgtt tccttttctc aattttctct 60

ttcgaatgac cgcattgaaa ttcaggctgc ccaacgcgtt tttgttttca caattaattt 120

ttgaatcata cgcgaagatc atgatgagaa tggttgtgga aaaaaactgt ttgtaaatat 180

ttag 184

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<210> SEQ ID NO 315
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 315

atatcacatt accattcaaa aaataaacat tttacaaaat acaattccat aacaattttc 60

ttccctgttc caacctccac aaaagtaaat gatcgtataa gaaattaact accaacaaaa 120

atcccaaagt taaaggaaga catccccaaa aaagatgtaa ctttcaaaac cggatgactt 180

cactcctgcc attgcaccta gtcatttact tctcagagga gtttggccct ttcttctttc 240

caaaagtaac cactgcggta acaaaccggc ggttgtattg cattcgcttg taggcgcggc 300

ctctaggctt cttcttctgt cttgtttggc caccttaggg tccgc 345

<210> SEQ ID NO 316
<211> LENGTH: 292
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 316

gcggacgcct tggtacaatg gacttgcaaa aataaaatga gttctcattt gtgggtgaga 60

tgcggatatt ttatgcatag gcacttcatg gagatgtggt ttataaacgc catcttaata 120

tctgtaccta ttactttcaa aatatgaagg caagatggaa agctactcat ctgttgtgaa 180

gtcagaatgt tggtagcggt tgggctctga aagtaagaaa ctttttgatt ggtttaatta 240

aatgagggaa tttgcctggt ttccctcttc cttccgaaaa aaaaaaaaaa aa 292

<210> SEQ ID NO 317
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 317

gacgttgtaa aacgacggcc agacaatatt ggaagggaga aaggcgccag cagggttgag 60

gggaagaaat gcataatgac atatataatg agatctattt gtatacgata ttacgggtac 120

gatcgatgat tcgagctacg atcccatacg acgctaaagc gtaattacat atataataga 180

tgcatttcag aatgacttat ctatttcatt acgcgatatt atatacgtaa ttacgtatat 240

aattgcagag atctcaccga ccaaccaaat agtctttcat ttcatcccag gcgtccgc 298

<210> SEQ ID NO 318
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 318

gcggacgcct gtatcactag aggtgaatac tcagcaagca aaactgaagg atattattga 60

aaaagctgtc aaggctaaat tgggtgtcaa ttccccattg atcatgcatg gttctacact 120

tttgtttgag tccggtgatg acattgagga agatgttgct gcacattatg cacaaaactt 180

agagaagacg ttagcagaat ttccagttcc aatcacaaat ggtgttattc ttacagtaga 240

ggactaccag caagagttct tatgcagtat taatattaag cacagagatg actttgatga 300

ggagtcaggt ggcattgtac tgtctggagg cgtccgc 337

<210> SEQ ID NO 319
<211> LENGTH: 237
<212> TYPE: DNA

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<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 319

gcggacgcct ccttgtagat accatacatg agtctaagat caaaatcata caagaagagc 60

ttcattccgg gcctcacctt ttctacaagc tccttttttgg ctggtggaaa gccaaacact 120

ctgtatcgga aacactcctg cctagtttca gaattacaca taaaaatcaa gccggcaaac 180

ctatctttgc cactgccatc ttcattgttt gcgtcctggc cgtcgtttta caacgtc 237

<210> SEQ ID NO 320
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 320

gcggacgcct tactaaaacg acggccagat gtgtaatggg gaaaatgtgt catgatagtt 60

gggtacaaat aacgagccac ctgctctatg ttttcgaagt tttctgttgg atttgtccgg 120

gtgagagagc gttcgttcgt tgcgcgagag gggcaaaatg ctgagcgtgg ggaattgcca 180

ttgccgcccc tggaagtgcc gcacgaacgc gatcacattt aaatcaccat ttacttcatc 240

atcaccatgg ttaaatgcag tccctgctcc ttcaaacagg aacttcagat ccttcaagct 300

cgaaatctcc gcctctgctt cctcgaagac aagactctgt gaggaggaag cgcagcagct 360

gagcttagcg gatctgctga agcccggtgg cctcgccccc gatgggttct cgtacaagga 420

gaactttacc atacgctgct atgaagtccg agttaaaccg cactgccacc attgaggcgt 480

ccgc 484

<210> SEQ ID NO 321
<211> LENGTH: 248
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 321

gacgttgtaa aacgacggcc agcaaccaaa taaaccccac atgtgctcaa tgttttagta 60

taaaaggaga tgacttaaga gtcatttcac acacacttct atcttgattt ctctccactt 120

gtcttgggtt ttagtggaag agaaatctag gagtggaagc cctagacgtt ggaggataag 180

aaggcaaccc tagaaggcag agctaacgct atcctaaggc aaccctaacg ctatcctaag 240

gcgtccgc 248

<210> SEQ ID NO 322
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 322

gcggacgcct gctcagcacc tgttatagtc atttcttttt tccttttttct cattttctc 60

tttcgaatga ccgcaatgaa attcaggctg cccaacgcgt ttttgttttc acaattaatt 120

tttgaatcat acgcgaagat catgatgaga atggttgtgg aaaaaaactg tttgtaaata 180

tttaggtgac caacaatttt catgattgca atctaaagtt gataattgat ttatcgggtc 240

gacatttgta attattaaca cggaaaatct gaggcttaca atttttggat tgtaaatatt 300

taggtgacga acaattttca tgattgcaat ctaaagttga caattgagtt atcgtgtcga 360

catttgtaat tattaacaca caaaatctat gaggcgtccg c 401

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<210> SEQ ID NO 323
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 323

gcggacgcct catcaatcca tggttgtaca cgcgccttca aagcggcttc cttatgtcgc 60

gcagcgtcta cttgttcctt gagcgctttt ccctgctaca tccgcgcgag cctctgtgca 120

agggccactg tctgcgcggt ccctttaact tcgtcgtact tctgctgcag ctcacgtgtc 180

tctatttcta agtgctatat atttgggtcc tcctgcatag tagtgaactt cgaacgactc 240

ctcaaatagc caggtgtagt ctttcattgc actattgatc tccactattc ctgctataat 300

ggcgctaaca tgctgttcct tcacctttgg cggagttgaa ggctgcgcct tcttggagct 360

cggttatttg aagctgaacc ttgggcatat cttccttcac ctcgtgcatc ccctgcttcg 420

agtttctgga tgcacgcctc cactgggtct tctgctggga tgggcaactc taagaccaac 480

tggtatgcgt cgc 493

<210> SEQ ID NO 324
<211> LENGTH: 143
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 324

gcggacgcct tcttcaatcc atcaggcctg attaatgtat tgaccttctt tgtctgaatg 60

tcatacattt ttttcactgc atccttgatc ttcttcttgt cttgctttct atcctttctc 120

ttgctttcta tcctttctct ggc 143

<210> SEQ ID NO 325
<211> LENGTH: 314
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 325

gacgttgtaa aacgacggcc agcaaaattg atataaagaa tagacacatc gactcaaatg 60

aagtgactca acagttcatt aattcatgtc agcttgaatg catggacata cacccataaa 120

taggcagttg gggtcaccca aaagaacata gaaacatctc gcatctctct gaagaaactc 180

ggatgggtac aggtctgtga cttcgcatat tttgaaggag cactctcttg gataagtaca 240

atataggtac catctcggac tcgcctgaaa tctcgcaaag aagtctcatt ctcctccttg 300

ttacaggcgt ccgc 314

<210> SEQ ID NO 326
<211> LENGTH: 332
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 326

gacgttgtaa aacgacggcc agaagcatca ataaacaaaa tgacagatta acaagttctc 60

tcttaatctt aagagaatac atcaacatcc aagtaaagtc ataacacatt tacaaaatgg 120

tgccacggta tccattctct gtaacaaggt ttttctgaaa atagttttcc tcttatctat 180

gtaactcttc atagggatgc ctgtgtcaac gtgccatatt cccaaatttg gccacaatca 240

aaccttcctc attagaagaa acaatctctg gtctagctca aaattggcaa aatttccagc 300

atctcccttt aacatcatta gaaggcgtcc gc 332

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<210> SEQ ID NO 327
<211> LENGTH: 1098
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (879)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 327

gggagatgct aatttgaagc ccttctctga aggtggacaa ttccagcagc agtggtctaa 60

agccccaata tggctataga aattcttctg ggggttgcac ctatggaaga gggtcggaga 120

ggacgaagct gtggatcgct cttaccatct gtgcggaagg tggtagcaga attcattgga 180

acgttcttcc tcatatttgt aggatgcgga tctgtcgttg ttgataagat aagcaacggt 240

tccataactc atcttggtgt gtcgcttgta tggggaatgg cggccatgat tgtaatttat 300

tccataggcc atatttctgg agctcatttg aatcctgcag tgacgttggc ccttgcggct 360

gtgaagagat ttccatgggt tcaggttcca ggctacatag tagctcaagt atttggatcg 420

atatctgctg ggtttctcct acgtttcatg tttggagaag tggcattcat gggagccaca 480

gttccttcag gctcagaaat gcagtctttc gctttggaaa ttattactac gtcattgttg 540

gtgtttgtgg tttctgcagt cgccactgat acaaaagcgg tgggtgaatt gggaggttca 600

gcaattggag cgaccatcgc aatgaatgta gccatatccg gaccaatctc aggagcttca 660

atgaatccag caaggacaat aggatccgca gtggctggca acaaatatac aagcatttgg 720

gtttacatgg ttgggcctgt aatcggtgcg ctaatgggtg caatgagtta taacatgatt 780

agagagacaa aaatgtccga aagggagatt atgaagagtg ggtcatttgt taaggacatg 840

ggctccagcg aatcaacagc ataacaactt agagatttnt tgcattcccg agacggtatc 900

cagtgatagt ggagagtagt cataataaga tttgtgaaaa tgtttgtgta gattaatgtg 960

taaaattcaa tccatcaacc atgaagcgaa ctgcattccg tttttaaatg tttattggat 1020

ttgaattaat aaacagctta tacgtgaaaa tccctacttt atgtacggaa aaaaaaaaaa 1080

aaaaaaaaaa aaaaaaaa 1098

<210> SEQ ID NO 328
<211> LENGTH: 992
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (762)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (774)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (778)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (808)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (828)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (849)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (881)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (898)

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<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (936)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (945)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (953)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (967)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (977)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (984)..(985)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 328

actatagggc acgcgtggtc gacggcccga gctggtatcc gatgaagcta gattcaatgg 60

ttcaagtcct atgaaagcta gattggagaa ttgcaaagaa atctaatctc cgttagttgt 120

cccaaccact gactcgcacc caatcagagt atattaaagt taaagattat ataaaggtaa 180

attgaacatt tataaaatct taaatgtatt tttagagtta aacattatat agaatattta 240

atgtagtata gatataataa aatattaaaa attaatttct ctttactatc aagtgaataa 300

aaataaaaaa taaatgtaag acaatataat aaaagacttg tttttagtgc atttttgga 360

ctcttcgtta ttgtgtggta ttgtgttatt taaactgatc tttttactgt atatatggat 420

gggttaccca tcaaacttgt gatttcaata aattcctccc ggattttaga gaaattagac 480

cataaaaact cacgaaaaaa attttagacc ataaaaactc acgaaaaaaa cttccccaaa 540

atcacgctaa aaacaactag ataaaaaaat acccatcttt gatgatgtgg atagtgacag 600

cctattccaa actatcacct aaattgtaag ttacatgcat aacacgatga cctcatctat 660

acgttgtgcc aaataaaggt atgaccgttc aaactaaaga atcaacgagc tccaacgcat 720

cttttgctgt ggggggattc tcacggctta acattcatgg anccgattac cttnctancc 780

aaccaagggt tttaacctgg aacaaatncc aaaccaatta ccagcttnac aaatcaaccg 840

agccgcccna ccgggatcat tttggtcaag tctcgaaaac nggcattggg tatatggnat 900

atggaattgg aattggatca atggtaacct tggganaagc ttaanttgga aanccctttt 960

ttttganggg ggccaanttc ccgnnccccc gg 992

<210> SEQ ID NO 329
<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (933)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (952)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (982)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 329

atactcaagc tatgcatcca acgcgttggg agctctccct atggtcgacc tgcaggcggc 60

cgcgaattca ctagtgatta gatggtaaga gcgatccaca gcttcgtcct ctccgaccct 120

cttccatagg tgcaaccccc agaagaattt ctatagccat attgaggctt tagaccactg 180

-continued

gtgctggaat tgtccacctt cagagaaggg cttcaaatta gcatctccaa gttacattga 240

tctattctat tcatatacat ataacaatgc tgcttcgaga ctgacaaaat gatccgttgg 300

cgctcgttga ttgttagctg taattgtttg gattgttcag ttaaagcctt gttggtagga 360

ggtaatcggt catgaatgtt agccgtgaga atcctcacag caaaagatgc gttggagctc 420

gttgattctt tagtttgaac ggtcatacct ttatttggca caacgtatag atgaggtcat 480

cgtgttatgc atgtaactta caatttaggt gatagtttgg aataggctgt cactatccac 540

atcatcaaag atgggtattt tttatctagt tgtttttagc gtgattttgg ggaagttttt 600

ttcgtgagtt tttatggtct aaaatttttt tcgtgagttt ttatggtcta atttctctaa 660

aatccgggag gaatttattg aaatcacaag tttgatgggt aacccatcca tatatacagt 720

aaaaagatca gtttaccagc ccgggccgtc gaccacgcgt gccctatagt aatcgaattc 780

ccgcggccgc catggcggcc gggagcatgc gacgtcgggc ccaattcgcc ctatagtgag 840

tcgtattaca attcactggc cgcgtttaca cgtcgtgact gggaaaccct gcgttaccac 900

ttaatcgctt gagcacatcc ccttttccag tgngtaaaac gaaaaggccc cnccatcgcc 960

tttcaaaaat tggcaactga angggaagga ccccct 996

<210> SEQ ID NO 330
<211> LENGTH: 1041
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (918)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (934)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (943)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (991)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (1009)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (1025)..(1026)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (1030)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 330

atactcaagc tatgcatcca acgcgttggg agctctccca tatggtcgac ctgcaggcgg 60

ccgcgaattc actagtgatt agatggtaag agcgatccac agcttcgtcc cctccgaccc 120

tcttccatag gtataaaacc cagaatttgg tgagcaggaa gaatttccat agccatattg 180

aggctttaca ccactgctgc tcgaattgtc caccttcaga gaagggcttc aaattagcat 240

ctccaagtta catggatcta ttctattcat atatttataa caatgctgct tcgagactga 300

caaaattatt tgttggcgct tgttcatcgt tagctgtaat ggtttggatt gttcagtgta 360

ggaccagccc gggccgtcga ccacgcgtgc cctatagtaa tcgaattccc gcggccgcca 420

tggcggccgg gagcatgcga cgtcgggccc aattcgccct atagtgagtc gtattacaat 480

tcactggccg tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat 540

cgccttgcag cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat 600

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cgcccttccc aacagttgcg cagcctgaat ggcgaatgga cgcgccctgt agcggcgcat 660

taagcgcggc gggtgtggtg gttacgcgca gcgtgaccgc tacacttgcc agcgccctag 720

cgcccgctcc tttcgctttc ttccttcctt tctcgccacg ttcgccggct ttccccgtca 780

agctctaaat cgggggcttc ctttagggtt ccgatttaat gctttacggc accctcgacc 840

ccaaaaaaac ttgattaggg gtgatgggtc acgtagtggg ccatcgccct tgatagacgg 900

tttttcgccc tttgacgntg gaagtccacg tttntttaat agngggactc ttggttcaaa 960

atgggacaac acttcaaacc ttttttgggg ntatttttt tgatttatna agggattttt 1020

gccgnntttn gggccttttg g 1041

<210> SEQ ID NO 331
<211> LENGTH: 993
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (939)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (952)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (965)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (973)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (993)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 331

atactcaagc tatgcatcca acgcgttggg agctctccct atggtcgacc tgcaggcggc 60

cgcgaattca ctagtgatta ctatagggca cgcgtggtcg acggccccgg ctggtttcaa 120

taaattcctc ccggatttta gagaaattag accataaaaa ctcacgaaaa aaattttaga 180

ccataaaaac tcacgaaaaa aacttcccca aaatcacgct aaaaacaact agataaaaaa 240

atacccatct ttgatgatgt ggatagtgac agcctattcc aaactatcac ctaaattgta 300

agttacatgc ataacacgat gacctcatct atacgttgtg ccaaataaag gtatgaccgt 360

tcaaactaaa gaatcaacga gctccaacgc atcttttgct gtgaggattc tcacggctaa 420

cattcatgac cgattacctc ctaccaacaa ggctttaact gaacaatcca aacaattaca 480

gctaacaatc aacgagcgcc aacggatcat tttgtcagtc tcgaagcagc attgttatat 540

gtatatgaat agaatagatc aatgtaactt ggagatgcta atttgaagcc cttctctgaa 600

ggtggacaat tccagcacca gtggtctaaa gcctcaatat ggctatagaa attcttctgg 660

gggttgcacc tatggaagag ggtcggagag gacgaagctg tggatgctct taccatctaa 720

tcgaattccc gcggccgcca tggcggccgg gagcatgcga cgtcgggccc aattcgccct 780

atagtgagtc gtattacaat tcactggccg tcgttttaca acgtcgtgac tgggaaaacc 840

ctggcgtacc caacttaatc gccttgcagc acatcccctt tcgcagctgg gtaatagcga 900

aaaggccgca cgatgccttc cacagtgcca actgatggng aaggaccccc tntcgggcat 960

taacncgggg ggngggggttc cccccggcct ccn 993

<210> SEQ ID NO 332
<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (994)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (998)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (1014)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 332

atactcaagc tatgcatcca acgcgttggg agctctccca tatggtcgac ctgcaggcgg 60

ccgcgaattc actagtgatt agatggtaag agcgatccac agcttcgtcc tctccgaccc 120

tcttccatag gtgcaacccc cagaagaatt tctatagcca tattgaggct ttagaccact 180

ggtgctggaa ttgtccacct tcagagaagg gcttcaaatt agcatctcca agttacattg 240

atctattcta ttcatataca tataacaatg ctgcttcgag actgacaaaa tgatccgttg 300

gcgctcgttg attgttagct gtaattgttt ggattgttca gttaaggcct tgttggtagg 360

aggtaatcgg tcatgaatgt tagccgtgag aatcctcaca gcaaaagatg cgtcggagct 420

cgttgattct ttagtttgaa cggtcatacc tttatttggc acaacgtata gatgaggtca 480

tcgtgttatg catgtaactt acaatttagg tgatagtttg gaataggctg tcactatcca 540

catcatcaaa gatgggtatt tttttatcta gttgttttta gcgtgatttt ggggaagttt 600

ttttcgtgag ttttttatggt ctaaaatttt tttcgtgagt ttttatggtc taatttctct 660

aaaatccggg aggaatttat tgaaatcaca agtttgatgg gtaacccatc catatataca 720

gtaaaaagat cagtttaaat aacacaatac cacacaataa cgaagagtcc aaaaaatgca 780

ctaaaaacaa gtcttttatt atattggctt acatttattt tttacttta ttcacttgga 840

tagtaaaaga gaaattaatt tttaatattt tattatatct atactacatt aaatattcta 900

tataatgtta actctaaaaa acatttaaga tttatatatg gtcaattacc cttatataat 960

ctttaacttt aaatccctga tgggggccaa taanggtngg gaaactaacg gaan 1014

<210> SEQ ID NO 333
<211> LENGTH: 640
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda

<400> SEQUENCE: 333

actatagggc acgcgtggtc gacggcccgg gctggtttca ataaattcct cccggatttt 60

agagaaatta gaccataaaa actcacgaaa aaaattttag accataaaaa ctcacgaaaa 120

aaacttcccc aaaatcacgc taaaaacaac tagataaaaa aatacccatc tttgatgatg 180

tggatagtga cagcctattc caaactatca cctaaattgt aagttacatg cataacacga 240

tgacctcatc tatacgttgt gccaaataaa ggtatgaccg ttcaaactaa agaatcaacg 300

agctccaacg catcttttgc tgtgaggatt ctcacggcta acattcatga ccgattacct 360

cctaccaaca aggctttaac tgaacaatcc aaacaattac agctaacaat caacgggcgc 420

caacggatca ttttgtcagc ctcgaagcag cattgttata tgtatatgaa tagaatagat 480

caatgtaact tggagatgct aatttgaagc ccttctctga aggtggacaa ttccagcacc 540

agtggtctaa agcctcaata tggctataga aattcttctg ggggttgcac ctatggaaga 600

gggtcggaga ggacgaagct gtggatcgct cttaccatct 640

<210> SEQ ID NO 334

-continued

<211> LENGTH: 1028
<212> TYPE: DNA
<213> ORGANISM: Pinus taeda
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (953)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (973)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (981)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (1002)
<223> OTHER INFORMATION: a, t, c, g, other or unknown
<221> NAME/KEY: modified_base
<222> LOCATION: (1004)
<223> OTHER INFORMATION: a, t, c, g, other or unknown

<400> SEQUENCE: 334

atactcaagc tatgcatcca acgcgttggg agctctccct atggtcgacc tgcaggcggc 60

cgcgaattca ctagtgatta gatggtaaga gcgatccaca gcttcgtcct ctccgaccct 120

cttccatagg tgcaaccccc agaagaattt ctatagccat attgaggctt tagaccactg 180

gtgctggaat tgtccacctt cagagaaggg cttcaaatta gcatctccaa gttacattga 240

tctattctat tcatatacat ataacaatgc tgcttcgaga ctgacaaaat gatccgttgg 300

cgctcgttga ttgttagctg taattgtttg gattgttcag ttaaggcctt gttggtagga 360

ggtaatcggt catgaatgtt agccgtgaga atcctcacag caaaagatgc gttggagctc 420

gttgactctt tagtttgaac ggtcatacct ttatttggca caacgtatag atgaggtcat 480

cgtgttatgc atgtaactta cagtttaggt gatagtttgg aataggctgt cactatccac 540

atcatcaaag atgggtattt ttttatctag ttgtttttag cgtgattttg gggaagtttt 600

tttcgtgagt ttttatggtc taaaattttt ttcgtgagtt tttatggtct aatttctcta 660

aaatccgaga ggaatttatt gaaaccagcc cgggccgtcg accacgcgtg ccctatagta 720

atcgaattcc cgcggccgcc atggcggccg ggagcatgcg acgtcgggcc caattcgccc 780

tatagtgagt cgtattacaa ttcactggcc gtcgttttac aacgtcgtga ctgggaaaac 840

cctgcgtacc cacttaatcg ccttggagca catccccctt tcgccagctg gcgtaatagc 900

gaagaggccc ggacccgatc ggcctttcc aacaaattgc gcaaccctga atngggaaat 960

gggccccccc ctnttaccgg ngcaattaaa ccccgggggg gngnggggt tccccccccc 1020

gtggacct 1028

<210> SEQ ID NO 335
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 335

aagctttttt tttttg 16

<210> SEQ ID NO 336
<211> LENGTH: 13
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 336

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aagcttgatt gcc 13

<210> SEQ ID NO 337
<211> LENGTH: 13
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 337

aagcttcgac tgt 13

<210> SEQ ID NO 338
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 338

ctcttaatta agtacgcggg 20

<210> SEQ ID NO 339
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Clone LPS-097

<400> SEQUENCE: 339

gggcacaaag ctccgcagcc tgagcgagcg tcattagctt gtcagtcgga accattaccc 60

ctttcctctt cgctggctag cgaatgatag ggaatgctag ccagcgaaca agattagagc 120

acagaaagta tagccagcga atcaacagca taacaactta gagatttctt gcattcccca 180

gacggtatca agtcatagtg gagaataatc ataataagat ttgtgaaaat gtttgtgtag 240

attaatgtgt aaaattcaat ccatcaacca tgaagtgaag tgcattccgt ttttaaatgt 300

ttattgtatt tgaatgaata aacagtttac acgcgaaaat ccctacttta tgtgcgtaca 360

aactatgatt tttttgcagt atataaaagt ttccactatc gtaattattt tccagatccg 420

tcttcttaac aacccgattt cctagcatcc atctgcgtgg aataaatcta ttgaattatt 480

aacccttgtg attggctaaa aaaaaaa 507

The invention claimed is:

1. A method of staging conifer embryos comprising:

a) detecting the expression in a conifer embryo of at least one RNA transcript wherein the RNA transcript is capable of hybridizing to at least one cDNA sequence of SEQ ID NO: 79 or 131; and

b) correlating the expression of said transcript to one or more embryonic stages.

2. The method of claim 1 wherein at least two RNA transcripts are detected or determined and correlated to one or more embryonic stages.

3. The method of claim 1 wherein expression of the at least one RNA transcript is analyzed by hybridization with at least one probe of sequence SEQ ID NO: 79 or 131.

4. The method of claim 1 wherein said cDNA sequence hybridizes under conditions of moderate stringency.

5. The method of claim 1 wherein expression of at least one RNA transcript is detected or determined by one or more of PCR, Northern Analysis, or in situ hybridization.

6. The method of claim 1 wherein expression of said at least two RNA transcripts are detected by a DNA array.

7. The method of claim 1 wherein said cDNA sequence hybridizes under conditions of high stringency.

* * * * *